GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 17:39:55 ; Search time 20 Seconds
(without alignments)
572.204 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATRQGKRPSKNLKARCSR.....ANNVVYKQYEDMVVESCGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	645	99.4	501	2	JC2347	growth/differentia
2	640	98.6	495	2	S43294	bone morphogenetic
3	639	98.5	501	2	A55452	cartilage-derived
4	543	83.7	125	2	S43295	bone morphogenetic
5	528	81.4	436	2	B55452	cartilage-derived
6	493	76.0	151	2	S43296	bone morphogenetic
7	353.5	54.5	461	2	S52408	SPDVR1 protein - s
8	347	53.5	393	2	S37073	bone morphogenetic
9	347	53.5	394	2	S45355	bone morphogenetic
10	347	53.5	396	1	BMHU2	bone morphogenetic
11	347	53.5	401	2	JH0689	bone morphogenetic
12	346	53.3	400	2	A49147	bone morphogenetic
13	346	53.3	405	2	I50608	bone morphogenetic
14	344	53.0	588	2	A26158	decapentaplegic pr
15	343	52.9	398	2	JH0688	bone morphogenetic
16	343	52.9	398	2	JH0687	bone morphogenetic
17	341	52.5	408	2	S38343	bone morphogenetic
18	341	52.5	420	2	I49541	bone morphogenetic
19	339	52.2	408	1	BMHU4	bone morphogenetic
20	338	52.1	408	2	S58791	bone morphogenetic
21	337	51.9	353	2	I50607	bone morphogenetic
22	333	51.3	207	2	S37618	vgr protein - rat
23	333	51.3	452	2	I49542	bone morphogenetic
24	333	51.3	454	1	BMHU5	bone morphogenetic
25	332	51.2	513	1	BMHU6	bone morphogenetic
26	331	51.0	408	2	JH0801	bone morphogenetic
27	330	50.8	313	2	I51284	bone morphogenetic
28	330	50.8	431	1	BMHU7	bone morphogenetic
29	329	50.7	510	2	A54798	Vg-1-related prote
30	328	50.5	426	2	JH0690	bone morphogenetic
31	327	50.4	430	2	JQ1184	osteogenic protein
32	317.5	48.9	402	2	A45056	osteogenic protein
33	313	48.2	360	2	A29619	Vg1 embryonic grow
34	306.5	47.2	365	2	T43286	cet-1 protein - Ca
35	304	46.8	455	2	A43918	TGF-beta-related p
36	303	46.7	427	2	A40735	TGF beta homolog d
37	283.5	43.7	366	2	A46607	growth/differentia
38	281	43.3	472	1	BMHU3	bone morphogenetic
39	279.5	43.1	360	2	I53032	bone morphogenetic
40	278.5	42.9	366	2	A45402	transforming growt
41	274	42.2	366	2	T03907	TGF-beta-related p
42	271.5	41.8	372	2	C39364	GDF-1 embryonic gr
43	268.5	41.4	476	2	JC4646	bone morphogenetic
44	264.5	40.8	357	2	A39364	GDF-1 embryonic gr
45	264.5	40.8	478	2	JC4838	bone morphogenetic

ALIGNMENTS

RESULT 1
JC2347
growth/differentiation factor 5 - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
C;Accession: JC2347
R;Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A;Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A;Reference number: JC2347; MUID:95071375; PMID:7980526
A;Accession: JC2347
A;Molecule type: DNA
A;Residues: 1-501 <HOE>
A;Cross-references: GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525
C;Genetics:
A;Gene: GDB:BMP9
A;Cross-references: GDB:433948
A;Introns: 211/1
C;Superfamily: inhibin
C;Keywords: glycoprotein
F;189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 4.6e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
```

RESULT 2
S43294
bone morphogenetic protein-related protein (GDF5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S43294
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43294
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <STO>
A;Cross-references: GB:U08337; NID:g488461; PIDN:AAA18778.1; PID:g488462
C;Superfamily: inhibin

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  Query Match             98.6%;  Score 640;  DB 2;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 1.5e-58;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 3
A55452
cartilage-derived morphogenetic protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
C;Accession: A55452
R;Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Biol. Chem. 269, 28227-28234, 1994
A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming growt
A;Reference number: A55452; MUID:95050604; PMID:7961761
A;Accession: A55452
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-501 <CHA>
A;Cross-references: GB:U13660; NID:g600731; PID:g600732
C;Genetics:
A;Gene: GDB:CDMP1
A;Cross-references: GDB:438940
C;Superfamily: inhibin

  Query Match             98.5%;  Score 639;  DB 2;  Length 501;
  Best Local Similarity   98.3%;  Pred. No. 1.9e-58;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 4
S43295
bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N;Alternate names: growth and differentiation factor 6
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C;Accession: S43295
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43295
A;Molecule type: DNA
A;Residues: 1-125 <STO>
A;Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
C;Genetics:
A;Gene: Gdf6
C;Superfamily: inhibin
F;1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F;6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

  Query Match             83.7%;  Score 543;  DB 2;  Length 125;
  Best Local Similarity   80.3%;  Pred. No. 3.7e-49;
  Matches   94;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |:| ||| |  : ||||| |||||::||||||||||||||:||||:|:||||||||||
Db          9 ASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPT 68

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||:|||||||||| |||| |||||:|:|||||:||: ||||||||||||||||||
Db         69 NHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 125


RESULT 5
B55452
cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
C;Accession: B55452
R;Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
J. Biol. Chem. 269, 28227-28234, 1994
A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming growt
A;Reference number: A55452; MUID:95050604; PMID:7961761
A;Accession: B55452
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-436 <CHA>
A;Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490
C;Superfamily: inhibin

  Query Match             81.4%;  Score 528;  DB 2;  Length 436;
  Best Local Similarity   76.9%;  Pred. No. 5.4e-47;
  Matches   90;  Conservative   16;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |:| ||| |  : |||:| |||||::||||||||||||||:||||:|:||||||||||
Db        320 ASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPT 379

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||:|||||||||| |||| |||||:|:|||||:||: ||||| :||:|||||||||
Db        380 NHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYNEYEEMVVESCGCR 436


RESULT 6
S43296
bone morphogenetic protein-related protein (GDF7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Accession: S43296
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <STO>
A;Cross-references: GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466
C;Superfamily: inhibin

  Query Match             76.0%;  Score 493;  DB 2;  Length 151;
  Best Local Similarity   73.5%;  Pred. No. 7.1e-44;
  Matches   83;  Conservative   20;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
              |:   :  ::|||||:|||:||::||||||||||:|||:||||:|:|||||||||||:
Db         39 GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 98

Qy         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:||| |:: | : ||| ||||||||:||:|||||||||||||:||||
Db         99 IQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR 151


RESULT 7
S52408
SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
```

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C;Accession: S52408
R;Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A;Description: SpDVR1, a member of the transforming growth factor-beta superfamily expre
A;Reference number: S52408
A;Accession: S52408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <PON>
A;Cross-references: EMBL:Z48313; NID:g673496; PID:g673497
C;Superfamily: inhibin

  Query Match             54.5%;  Score 353.5;  DB 2;  Length 461;
  Best Local Similarity   48.1%;  Pred. No. 7.3e-29;
  Matches   65;  Conservative   19;  Mismatches   32;  Indels   19;  Gaps    2;

Qy          3 ATRQ---GKRPSK----------------NLKARCSRKALHVNFKDMGWDDWIIAPLEYE 43
              ||||   |||| |                |   :| || | |||:|: | :|||||| |
Db        326 ATRQKKGGKRPRKPDTDNDIASRDSASSLNSDWQCKRKNLFVNFEDLDWQEWIIAPLGYV 385

Qy         44 AFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNV 103
              ||:|:| | |||  |   ||||::|||:: | |   |   | ||:||||::|: | : ||
Db        386 AFYCQGECAFPLNGHANATNHAIVQTLVHHMSPSHVPQPCCAPTKLSPITVLYYDDSRNV 445

Qy        104 VYKQYEDMVVESCGC 118
              | |:|::||| :|||
Db        446 VLKKYKNMVVRACGC 460


RESULT 8
S37073
bone morphogenetic protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S37073
R;Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993
A;Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protei
A;Reference number: S37073
A;Accession: S37073
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-393 <FEN>
A;Cross-references: EMBL:Z25868; NID:g397950; PIDN:CAA81088.1; PID:g397951
C;Superfamily: inhibin

  Query Match             53.5%;  Score 347;  DB 2;  Length 393;
  Best Local Similarity   54.3%;  Pred. No. 2.9e-28;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| |' | |||  ||  ||
Db        279 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 338

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        339 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 393


RESULT 9
S45355
bone morphogenetic protein-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C;Accession: S45355
R;Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1218, 221-224, 1994
A;Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comp
A;Reference number: S45355; MUID:94289485; PMID:8018727
A;Accession: S45355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <FEN>
C;Superfamily: inhibin

  Query Match             53.5%;  Score 347;  DB 2;  Length 394;
  Best Local Similarity   54.3%;  Pred. No. 2.9e-28;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| |' | |||  ||  ||
Db        280 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 339

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        340 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 394


RESULT 10
BMHU2
bone morphogenetic protein 2 precursor - human
N;Alternate names: bone morphogenetic protein 2A; rhBMP2
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: B37278; PC2178
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He
Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730; PMID:3201241
A;Accession: B37278
A;Molecule type: mRNA
A;Residues: 1-396 <WO2>
A;Cross-references: GB:M22489; NID:g179501; PIDN:AAA51834.1; PID:g179502
R;Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Katay
J. Biochem. 115, 279-285, 1994
A;Title: Expression and characterization of human bone morphogenetic protein-2 in silkw
A;Reference number: PC2178; MUID:94266754; PMID:8206877
A;Accession: PC2178
A;Molecule type: protein
A;Residues: 290-295,'X',297-304 <ISH>
A;Experimental source: cell line BoMo-15AIIc
R;Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.
Protein Sci. 4(Suppl.2), 443S, 1995
A;Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2)
A;Reference number: A56729
A;Contents: annotation
A;Note: determination of amino ends of mature forms; dimers with long form chains have
C;Comment: This hormone is capable of inducing bone formation at ectopic morphological
C;Genetics:
A;Gene: GDB:BMP2; BMP2A
A;Cross-references: GDB:125204; OMIM:112261
A;Map position: 20p12-20p12
C;Complex: homodimer, disulfide linked
C;Superfamily: inhibin
C;Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-265/Domain: propeptide #status predicted <PRO>
F;266-396/Product: bone morphogenetic protein 2, long form #status predicted <MATL>
F;283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>
F;135,163,164,200/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim
F;338/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             53.5%;  Score 347;  DB 1;  Length 396;
  Best Local Similarity   54.3%;  Pred. No. 2.9e-28;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| |' | |||  ||  ||
Db        282 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 341

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        342 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 396
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RESULT 11
JH0689
bone morphogenetic protein 4 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: JH0689
R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A;Reference number: JH0687; MUID:92378616; PMID:1510675
A;Accession: JH0689
A;Molecule type: mRNA
A;Residues: 1-401 <NIS>
A;Cross-references: GB:X63426; NID:g64587; PIDN:CAA45020.1; PID:g64588
A;Experimental source: oocyte
C;Superfamily: inhibin
C;Keywords: glycoprotein
F;288-401/Product: bone morphogenetic protein 4 #status predicted <MAT>
F;141,204,238,343,358/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             53.5%;  Score 347;  DB 2;  Length 401;
  Best Local Similarity   52.1%;  Pred. No. 3e-28;
  Matches   63;  Conservative   21;  Mismatches   31;  Indels    6;  Gaps    2;

Qy          4 TRQGKRPSKNLKAR-----CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH 58
              ||: ||  |  : |     | | :|:|:| |:||:|||:||  |:||:| | | |||  |
Db        282 TRRSKRSPKQQRPRKKNKHCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADH 341

Qy         59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGC 118
              |  ||||::|||:||::  | |   |||| || ||:|::|  : || | |::|||| |||
Db        342 LNSTNHAIVQTLVNSVN-SSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC 400

Qy        119 R 119
              |
Db        401 R 401


RESULT 12
A49147
bone morphogenetic protein 4 - African clawed frog
N;Alternate names: BMP-4; ventralizing factor
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A49147
R;Dale, L.; Howes, G.; Price, B.M.; Smith, J.C.
Development 115, 573-585, 1992
A;Title: Bone morphogenetic protein 4: a ventralizing factor in early Xenopus developmen
A;Reference number: A49147; MUID:93048819; PMID:1425340
A;Accession: A49147
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-400 <DAL>
A;Cross-references: GB:X64538; GB:S46999; NID:g64589; PIDN:CAA45836.1; PID:g64590
A;Experimental source: XTC cells
A;Note: sequence extracted from NCBI backbone (NCBIN:117127, NCBIP:117128)
C;Superfamily: inhibin

  Query Match             53.3%;  Score 346;  DB 2;  Length 400;
  Best Local Similarity   52.1%;  Pred. No. 3.8e-28;
  Matches   63;  Conservative   21;  Mismatches   31;  Indels    6;  Gaps    2;

Qy          4 TRQGKRPSKNLKAR-----CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH 58
              ||: ||  |  : |     | | :|:|:| |:||:|||:||  |:||:| | | |||  |
Db        281 TRRSKRSPKQQRPRKKNKHCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADH 340

Qy         59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGC 118
              |  ||||::|||:||::  | |   |||| || ||:|::|  : || | |::|||| |||
Db        341 LNSTNHAIVQTLVNSVN-ASIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC 399

Qy        119 R 119
              |
Db        400 R 400


RESULT 13
I50608
bone morphogenetic protein 4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I50608
R;Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
Development 120, 209-218, 1994
A;Title: Bone morphogenetic proteins and a signalling pathway that controls patterning :
A;Reference number: I50607; MUID:94163974; PMID:8119128
A;Accession: I50608
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-405 <FRA>
A;Cross-references: EMBL:X75915; NID:g472929; PIDN:CAA53514.1; PID:g472930
C;Genetics:
A;Gene: Bmp-4
C;Superfamily: inhibin

  Query Match             53.3%;  Score 346;  DB 2;  Length 405;
  Best Local Similarity   52.1%;  Pred. No. 3.8e-28;
  Matches   63;  Conservative   21;  Mismatches   31;  Indels    6;  Gaps    2;

Qy          4 TRQGKRP-----SKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH 58
              ||: :|      |:  |  | | ||:|:| |:||:|||:||  |:||:| | | |||  |
Db        286 TRRARRSPKHHGSRKNKKNCRRHALYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADH 345

Qy         59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGC 118
              |  ||||::|||:||::  | |   |||| || ||:|::|  : || | |::|||| |||
Db        346 LNSTNHAIVQTLVNSVN-SSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC 404

Qy        119 R 119
              |
Db        405 R 405


RESULT 14
A26158
decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
C;Accession: A26158
R;Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
Nature 325, 81-84, 1987
A;Title: A transcript from a Drosophila pattern gene predicts a protein homologous to tl
A;Reference number: A26158; MUID:87090408; PMID:3467201
A;Accession: A26158
A;Molecule type: mRNA
A;Residues: 1-588 <PAD>
A;Cross-references: GB:M30116; NID:g157291; PID:g157292
C;Genetics:
A;Gene: FlyBase:dpp
A;Cross-references: FlyBase:FBgn0000490
C;Keywords: glycoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             53.0%;  Score 344;  DB 2;  Length 588;
  Best Local Similarity   48.7%;  Pred. No. 9.3e-28;
  Matches   57;  Conservative   24;  Mismatches   34;  Indels    2;  Gaps    1;

Qy          5 RQGKRPS--KNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |  :||:  ||     | | :|:|:| |:||||||:||| |:|::| | | |||  |   |
Db        472 RHARRPTRRKNHDDTCRRHSLYVDFSDVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST 531

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:|||:|:|:|   |  ||||:|  :::|:::  : || | |::| |  ||||
Db        532 NHAVVQTLVNNMNPGKVPKACCVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVGCGCR 588


RESULT 15
JH0688
```

bone morphogenetic protein 2II precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: JH0688
R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A;Reference number: JH0687; MUID:92378616; PMID:1510675
A;Accession: JH0688
A;Molecule type: mRNA
A;Residues: 1-398 <NIS>
A;Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
A;Experimental source: oocyte
C;Superfamily: inhibin
C;Keywords: glycoprotein
F;285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F;137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.9%; Score 343; DB 2; Length 398;
Best Local Similarity 53.4%; Pred. No. 7.6e-28;
Matches 62; Conservative 19; Mismatches 33; Indels 2; Gaps 2;

```
Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              ||  : :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        284 RQARHKQRKRLKSSCRRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 343

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::  : |   |||| || ||:|::|    || | |:||||| ||||
Db        344 HAIVQTLVNSVN-TNIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 398
```

Search completed: February 18, 2004, 17:43:53
Job time : 21 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 17:38:15 ; Search time 14 Seconds
(without alignments)
399.727 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATRQGKRPSKNLKARCSR.....ANNVVYKQYEDMVVESCGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	645	99.4	501	1	GDF5_HUMAN	P43026 homo sapien
2	640	98.6	495	1	GDF5_MOUSE	P43027 mus musculu
3	543	83.7	125	1	GDF6_MOUSE	P43028 mus musculu
4	528	81.4	436	1	GDF6_BOVIN	P55106 bos taurus
5	493	76.0	151	1	GDF7_MOUSE	P43029 mus musculu
6	353.5	54.5	461	1	DVR1_STRPU	P48969 strongyloce
7	352	54.2	395	1	UNIV_STRPU	P48970 strongyloce
8	347	53.5	393	1	BMP2_RAT	P49001 rattus norv
9	347	53.5	394	1	BMP2_MOUSE	P21274 mus musculu
10	347	53.5	395	1	BMP2_RABIT	O46564 oryctolagus
11	347	53.5	396	1	BMP2_DAMDA	O19006 dama dama (
12	347	53.5	396	1	BMP2_HUMAN	P12643 homo sapien
13	347	53.5	401	1	BMP4_XENLA	P30885 xenopus lae
14	347	53.5	593	1	DECA_DROSI	P91706 drosophila
15	346	53.3	405	1	BMP4_CHICK	Q90752 gallus gall
16	344	53.0	588	1	DECA_DROME	P07713 drosophila
17	343	52.9	398	1	BMPA_XENLA	P25703 xenopus lae
18	343	52.9	398	1	BMPB_XENLA	P30884 xenopus lae
19	341	52.5	408	1	BMP4_MOUSE	P21275 mus musculu
20	341	52.5	408	1	BMP4_RAT	Q06826 rattus norv
21	339	52.2	408	1	BMP4_HUMAN	P12644 homo sapien
22	338	52.1	372	1	DECA_TRICA	Q26974 tribolium c
23	338	52.1	408	1	BMP4_DAMDA	Q29607 dama dama (
24	337	51.9	353	1	BMP2_CHICK	Q90751 gallus gall
25	336	51.8	409	1	BMP4_RABIT	O46576 oryctolagus
26	335	51.6	355	1	DVR1_BRARE	P35621 brachydanio
27	334	51.5	621	1	DECA_DROPS	P91699 drosophila
28	333	51.3	207	1	BMP6_RAT	Q04906 rattus norv
29	333	51.3	452	1	BMP5_MOUSE	P49003 mus musculu
30	333	51.3	454	1	BMP5_HUMAN	P22003 homo sapien
31	332	51.2	513	1	BMP6_HUMAN	P22004 homo sapien
32	330	50.8	431	1	BMP7_HUMAN	P18075 homo sapien
33	329	50.7	510	1	BMP6_MOUSE	P20722 mus musculu
34	328	50.5	426	1	BMP7_XENLA	P30886 xenopus lae
35	327	50.4	430	1	BMP7_MOUSE	P23359 mus musculu
36	317.5	48.9	402	1	BMP8_HUMAN	P34820 homo sapien
37	314.5	48.5	399	1	BM8A_MOUSE	P34821 mus musculu
38	313	48.2	360	1	DVR1_XENLA	P09534 xenopus lae
39	304	46.8	455	1	60A_DROME	P27091 drosophila
40	303	46.7	427	1	DSL1_CHICK	P34822 gallus gall
41	302	46.5	436	1	60A_DROVI	Q24735 drosophila
42	300.5	46.3	424	1	BM10_HUMAN	O95393 homo sapien
43	297.5	45.8	420	1	BM10_MOUSE	Q9r229 mus musculu
44	293.5	45.2	428	1	GDF2_MOUSE	Q9wv56 mus musculu
45	291.5	44.9	364	1	GDF3_HUMAN	Q9nr23 homo sapien

ALIGNMENTS

RESULT 1
GDF5_HUMAN
ID GDF5_HUMAN STANDARD; PRT; 501 AA.
AC P43026; Q96SB1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Growth/differentiation factor 5 precursor (GDF-5) (Cartilage-derived
DE morphogenetic protein 1) (CDMP-1).
GN GDF5 OR CDMP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95071375; PubMed=7980526;
RA Hoetten G., Neidhardt H., Jacobowsky B., Pohl J.;
RT "Cloning and expression of recombinant human growth/differentiation
RT factor 5.";
RL Biochem. Biophys. Res. Commun. 204:646-652(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed
RT in long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

```
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
CC       HUMAN EMBRYONIC DEVELOPMENT.
CC   -!- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC
CC       CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
CC       DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
CC       RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
CC       METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE
CC       PHALANGES ARE ALMOST SQUARE.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80915; CAA56874.1; -.
DR   EMBL; U13660; AAA57007.1; -.
DR   EMBL; AL121586; CAB89416.1; -.
DR   EMBL; BC032495; AAH32495.1; -.
DR   PIR; A55452; A55452.
DR   PIR; JC2347; JC2347.
DR   HSSP; P12643; 3BMP.
DR   Genew; HGNC:4220; GDF5.
DR   MIM; 601146; -.
DR   MIM; 201250; -.
DR   MIM; 200700; -.
DR   GO; GO:0008083; F:growth factor activity; TAS.
DR   GO; GO:0005515; F:protein binding activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007179; P:TGFbeta receptor signaling pathway; TAS.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Glycoprotein; Dwarfism.
FT   SIGNAL       1     27       POTENTIAL.
FT   PROPEP      28    381       POTENTIAL.
FT   CHAIN      382    501       GROWTH/DIFFERENTIATION FACTOR 5.
FT   DISULFID   400    466       BY SIMILARITY.
FT   DISULFID   429    498       BY SIMILARITY.
FT   DISULFID   433    500       BY SIMILARITY.
FT   DISULFID   465    465       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    38     38       T -> S (IN REF. 2).
FT   CONFLICT   254    258       APGGG -> VPRSR (IN REF. 2).
FT   CONFLICT   276    276       S -> A (IN REF. 2).
FT   CONFLICT   321    321       A -> T (IN REF. 2).
FT   CONFLICT   384    384       L -> S (IN REF. 2).
SQ   SEQUENCE   501 AA;  55410 MW;  37985F2D15C4F5EF CRC64;

  Query Match             99.4%;  Score 645;  DB 1;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1.2e-61;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 2
GDF5_MOUSE
ID   GDF5_MOUSE     STANDARD;      PRT;   495 AA.
AC   P43027;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Growth/differentiation factor 5 precursor (GDF-5).
GN   GDF5 OR GDF-5 OR BP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD-1; TISSUE=Embryo;
RX   MEDLINE=94195427; PubMed=8145850;
RA   Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA   Lee S.-J.;
RT   "Limb alterations in brachypodism mice due to mutations in a new
RT   member of the TGF beta-superfamily.";
RL   Nature 368:639-643(1994).
CC   -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH
CC       ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE
CC       AXIAL SKELETON.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08337; AAA18778.1; -.
DR   PIR; S43294; S43294.
DR   HSSP; P12643; 3BMP.
DR   MGD; MGI:95688; Gdf5.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
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DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.
FT   SIGNAL       1     27       POTENTIAL.
FT   PROPEP      28    375       POTENTIAL.
FT   CHAIN      376    495       GROWTH/DIFFERENTIATION FACTOR 5.
FT   DISULFID   394    460       BY SIMILARITY.
FT   DISULFID   423    492       BY SIMILARITY.
FT   DISULFID   427    494       BY SIMILARITY.
FT   DISULFID   459    459       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     98     98       S -> P.
SQ   SEQUENCE   495 AA;  54885 MW;  CD0D5DE48185D2E3 CRC64;

  Query Match             98.6%;  Score 640;  DB 1;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 4e-61;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 3
GDF6_MOUSE
ID   GDF6_MOUSE     STANDARD;      PRT;   125 AA.
AC   P43028;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN   GDF6 OR GDF-6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=94195427; PubMed=8145850;
RA   Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA   Lee S.-J.;
RT   "Limb alterations in brachypodism mice due to mutations in a new
RT   member of the TGF beta-superfamily.";
RL   Nature 368:639-643(1994).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08338; AAA18779.1; -.
DR   PIR; S43295; S43295.
DR   HSSP; P12643; 3BMP.
DR   MGD; MGI:95689; Gdf6.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Glycoprotein.
FT   NON_TER      1      1
FT   PROPEP      <1      5       POTENTIAL.
FT   CHAIN        6    125       GROWTH/DIFFERENTIATION FACTOR 6.
FT   DISULFID    24     90       BY SIMILARITY.
FT   DISULFID    53    122       BY SIMILARITY.
FT   DISULFID    57    124       BY SIMILARITY.
FT   DISULFID    89     89       INTERCHAIN (BY SIMILARITY).
SQ   SEQUENCE   125 AA;  14373 MW;  10FA2A5B7748DA32 CRC64;

  Query Match             83.7%;  Score 543;  DB 1;  Length 125;
  Best Local Similarity   80.3%;  Pred. No. 2e-51;
  Matches   94;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |:| ||| | : ||||| ||||||::||||||||||||||:||||:|:||||||||||
Db          9 ASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPT 68

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||:|||||||||| |||| |||||:|:|||||:||: ||||||||||||||||||
Db         69 NHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 125


RESULT 4
GDF6_BOVIN
ID   GDF6_BOVIN     STANDARD;      PRT;   436 AA.
AC   P55106;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
DE   morphogenetic protein 2) (CDMP-2) (Fragment).
GN   GDF6 OR CDMP2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Articular cartilage;
RX   MEDLINE=95050604; PubMed=7961761;
RA   Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA   Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT   "Cartilage-derived morphogenetic proteins. New members of the
RT   transforming growth factor-beta superfamily predominantly expressed
RT   in long bones during human embryonic development.";
RL   J. Biol. Chem. 269:28227-28234(1994).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U13661; AAA61416.1; -.
DR   PIR; B55452; B55452.
DR   HSSP; P18075; 1BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Glycoprotein.
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FT   NON_TER       1      1
FT   PROPEP       <1    316       POTENTIAL.
FT   CHAIN       317    436       GROWTH/DIFFERENTIATION FACTOR 6.
FT   DISULFID    335    401       BY SIMILARITY.
FT   DISULFID    364    433       BY SIMILARITY.
FT   DISULFID    368    435       BY SIMILARITY.
FT   DISULFID    400    400       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   436 AA;  47873 MW;  B0688E12EF8AE91D CRC64;

  Query Match             81.4%;  Score 528;  DB 1;  Length 436;
  Best Local Similarity   76.9%;  Pred. No. 3.6e-49;
  Matches   90;  Conservative   16;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |:| |||   |   : |||:| ||||||::|||||||||||||||:||||:|:||||||||||
Db        320 ASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPT 379

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||:|||||||||| |||| |||||:|:|||||:|| ||||| :||:|||||||||
Db        380 NHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYNEYEEMVVESCGCR 436


RESULT 5
GDF7_MOUSE
ID   GDF7_MOUSE     STANDARD;      PRT;   151 AA.
AC   P43029;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Growth/differentiation factor 7 precursor (GDF-7) (Fragment).
GN   GDF7 OR GDF-7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=94195427; PubMed=8145850;
RA   Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA   Lee S.-J.;
RT   "Limb alterations in brachypodism mice due to mutations in a new
RT   member of the TGF beta-superfamily.";
RL   Nature 368:639-643(1994).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U08339; AAA18780.1; -.
DR   PIR; S43296; S43296.
DR   HSSP; P12643; 3BMP.
DR   MGD; MGI:95690; Gdf7.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Glycoprotein.
FT   NON_TER       1      1
FT   PROPEP       <1      5       POTENTIAL.
FT   CHAIN         6    151       GROWTH/DIFFERENTIATION FACTOR 7.
FT   DISULFID     50    116       BY SIMILARITY.
FT   DISULFID     79    148       BY SIMILARITY.
FT   DISULFID     83    150       BY SIMILARITY.
FT   DISULFID    115    115       INTERCHAIN (BY SIMILARITY).
FT   DOMAIN        1      5       POLY-ARG.
FT   DOMAIN       16     41       POLY-GLY.
SQ   SEQUENCE   151 AA;  15697 MW;  0E496AACB5827759 CRC64;

  Query Match             76.0%;  Score 493;  DB 1;  Length 151;
  Best Local Similarity   73.5%;  Pred. No. 5.9e-46;
  Matches   83;  Conservative   20;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
              |:   :  ::|||||:|||:||::||||||||||:|||:||||:|:||||||||||||:
Db         39 GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 98

Qy         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:||| |:: | : ||| |||||||||:||:||||||||||||:||||
Db         99 IQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR 151


RESULT 6
DVR1_STRPU
ID   DVR1_STRPU     STANDARD;      PRT;   461 AA.
AC   P48969;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DVR-1 protein homolog precursor.
GN   DVR1.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ponce M.R., Micol J.L., Davidson E.H.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z48313; CAA88306.1; -.
DR   PIR; S52408; S52408.
DR   HSSP; P18075; 1BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   PROPEP       31    338       POTENTIAL.
FT   CHAIN       339    461       DVR-1 PROTEIN HOMOLOG.
FT   DISULFID    360    426       BY SIMILARITY.
FT   DISULFID    389    458       BY SIMILARITY.
FT   DISULFID    393    460       BY SIMILARITY.
FT   DISULFID    425    425       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    402    402       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  51881 MW;  2573D54B6625F7EF CRC64;
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  Query Match           54.5%;  Score 353.5;  DB 1;  Length 461;
  Best Local Similarity  48.1%;  Pred. No. 2.1e-30;
  Matches   65;  Conservative   19;  Mismatches   32;  Indels   19;  Gaps    2;

Qy          3 ATRQ---GKRPSK----------------NLKARCSRKALHVNFKDMGWDDWIIAPLEYE 43
              ||||   |||| |                |   :| || | |||:|: | :|||||| |
Db        326 ATRQKKGGKRPRKPDTDNDIASRDSASSLNSDWQCKRKNLFVNFEDLDWQEWIIAPLGYV 385

Qy         44 AFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNV 103
              ||:|:| | |||   |   ||||::|||:: | |   |   | ||:||||::|: | : ||
Db        386 AFYCQGECAFPLNGHANATNHAIVQTLVHHMSPSHVPQPCCAPTKLSPITVLYYDDSRNV 445

Qy        104 VYKQYEDMVVESCGC 118
              | |:|::||| :|||
Db        446 VLKKYKNMVVRACGC 460


RESULT 7
UNIV_STRPU
ID   UNIV_STRPU     STANDARD;      PRT;   395 AA.
AC   P48970;
DT   01-FEB-1996 (Rel. 33, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Univin precursor.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95046897; PubMed=7958442;
RA   Stenzel P., Angerer L.M., Smith B.J., Angerer R.C., Vale W.W.;
RT   "The univin gene encodes a member of the transforming growth
RT   factor-beta superfamily with restricted expression in the sea urchin
RT   embryo.";
RL   Dev. Biol. 166:149-158(1994).
RN   [2]
RP   REVISIONS TO N-TERMINUS.
RA   Angerer L.M., Stenzel P.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: COULD HAVE A CRITICAL ROLE IN EARLY DEVELOPMENTAL
CC       DECISIONS IN THE SEA URCHIN EMBRYO.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC   -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS OF EXPRESSION IN THE EGG AND
CC       PREHATCHING BLASTULA. DURING LATE CLEAVAGE STAGES, IT ACCUMULATES
CC       PROGRESSIVELY TO A CIRCUMEQUATORIAL BAND. DURING GASTRULATION IT
CC       IS DETECTED PRIMARILY IN THE PRESUMPTIVE FOREGUT AND CILIATED
CC       BAND. BY PLUTEUS STAGE, IT IS DETECTED ONLY IN THESE CELL TYPES.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U10533; AAA57553.2; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   PROPEP      20    272       POTENTIAL.
FT   CHAIN      273    395       UNIVIN.
FT   DISULFID   294    360       BY SIMILARITY.
FT   DISULFID   323    392       BY SIMILARITY.
FT   DISULFID   327    394       BY SIMILARITY.
FT   DISULFID   359    359       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    50     50       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   336    336       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   395 AA;  43837 MW;  0FA3340DF5A6360E CRC64;

  Query Match           54.2%;  Score 352;  DB 1;  Length 395;
  Best Local Similarity  54.5%;  Pred. No. 2.5e-30;
  Matches   60;  Conservative   22;  Mismatches   28;  Indels    0;  Gaps    0;

Qy         10 PSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQT 69
              |: :|   | |  | |:|:|:||::|||||: |:|::|:| | |||   |  ||||:|||
Db        286 PTASLTNLCQRHRLFVSFRDVGWENWIIAPMGYQAYYCDGECPFPLGERLNGTNHAIIQT 345

Qy         70 LMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |:||:|  :|   | ||:|| ||:|: |:  ||| :|||||||:||||
Db        346 LVNSIDNRAVPKVCCAPTKLSGISMLYFDNNENVVLRQYEDMVVEACGCR 395


RESULT 8
BMP2_RAT
ID   BMP2_RAT       STANDARD;      PRT;   393 AA.
AC   P49001;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN   BMP2 OR BMP-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone;
RA   Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
RL   Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z25868; CAA81088.1; -.
DR   PIR; S37073; S37073.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL       1     19       POTENTIAL.
FT   PROPEP      20    279
FT   CHAIN      280    393       BONE MORPHOGENETIC PROTEIN 2.
FT   DISULFID   293    358       BY SIMILARITY.
FT   DISULFID   322    390       BY SIMILARITY.
FT   DISULFID   326    392       BY SIMILARITY.
FT   DISULFID   357    357       INTERCHAIN (BY SIMILARITY).
```

```
FT   CARBOHYD    133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    335    335       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   393 AA;  44383 MW;  7D20865852E0F213 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 393;
  Best Local Similarity   54.3%;  Pred. No. 8.7e-30;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        279 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 338

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        339 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 393


RESULT 9
BMP2_MOUSE
ID   BMP2_MOUSE     STANDARD;      PRT;   394 AA.
AC   P21274;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN   BMP2 OR BMP-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94289485; PubMed=8018727;
RA   Feng J.Q., Harris M.A., Ghosh-Choudhury N., Feng M., Mundy G.R.,
RA   Harris S.E.;
RT   "Structure and sequence of mouse bone morphogenetic protein-2 gene
RT   (BMP-2): comparison of the structures and promoter regions of BMP-2
RT   and BMP-4 genes.";
RL   Biochim. Biophys. Acta 1218:221-224(1994).
RN   [2]
RP   SEQUENCE OF 1-351 FROM N.A.
RX   MEDLINE=90228966; PubMed=1970330;
RA   Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
RA   Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
RA   Siracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
RA   Jenkins N.A.;
RT   "Chromosomal localization of seven members of the murine TGF-beta
RT   superfamily suggests close linkage to several morphogenetic mutant
RT   loci.";
RL   Genomics 6:505-520(1990).
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L25602; AAB05665.1; -.
DR   PIR; A34201; A34201.
DR   HSSP; P12643; 3BMP.
DR   MGD; MGI:88177; Bmp2.
DR   GO; GO:0045165; P:cell fate commitment; IMP.
DR   GO; GO:0009790; P:embryonic development; IMP.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20    280
FT   CHAIN       281    394       BONE MORPHOGENETIC PROTEIN 2.
FT   DISULFID    294    359       BY SIMILARITY.
FT   DISULFID    323    391       BY SIMILARITY.
FT   DISULFID    327    393       BY SIMILARITY.
FT   DISULFID    358    358       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    162    162       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    336    336       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    110    110       T -> S (IN REF. 2).
FT   CONFLICT    113    114       QL -> HE (IN REF. 2).
FT   CONFLICT    271    271       G -> R (IN REF. 2).
SQ   SEQUENCE   394 AA;  44514 MW;  FD6A0F10587EED54 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 394;
  Best Local Similarity   54.3%;  Pred. No. 8.7e-30;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        280 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 339

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        340 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 394


RESULT 10
BMP2_RABIT
ID   BMP2_RABIT     STANDARD;      PRT;   395 AA.
AC   O46564;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 2 precursor (BMP-2).
GN   BMP2 OR BMP-2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Ocular ciliary epithelium;
RA   Wan X.L., Sears J., Chen S., Sears M.;
RT   "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
RT   epithelium.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF041421; AAB96785.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
```

```
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL        1     23       POTENTIAL.
FT   PROPEP       24    281       BY SIMILARITY.
FT   CHAIN       282    395       BONE MORPHOGENETIC PROTEIN 2.
FT   DISULFID    295    360       BY SIMILARITY.
FT   DISULFID    324    392       BY SIMILARITY.
FT   DISULFID    328    394       BY SIMILARITY.
FT   DISULFID    359    359       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    199    199       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   395 AA;  44664 MW;  8D1DDCFBAC582496 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 395;
  Best Local Similarity   54.3%;  Pred. No. 8.8e-30;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        281 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 340

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:||||| ||||
Db        341 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 395


RESULT 11
BMP2_DAMDA
ID   BMP2_DAMDA     STANDARD;      PRT;   396 AA.
AC   O19006;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 2 precursor (BMP-2).
GN   BMP2.
OS   Dama dama (Fallow deer) (Cervus dama).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=30532;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Antler;
RX   MEDLINE=97157076; PubMed=9003457;
RA   Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
RA   Harris S.E.;
RT   "Bone morphogenetic protein 2 transcripts in rapidly developing deer
RT   antler tissue contain an extended 5' non-coding region arising from a
RT   distal promoter.";
RL   Biochim. Biophys. Acta 1350:47-52(1997).
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001817; CAA05033.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
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DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL        1     23       POTENTIAL.
FT   PROPEP       24    282       BY SIMILARITY.
FT   CHAIN       283    396       BONE MORPHOGENETIC PROTEIN 2.
FT   DISULFID    296    361       BY SIMILARITY.
FT   DISULFID    325    393       BY SIMILARITY.
FT   DISULFID    329    395       BY SIMILARITY.
FT   DISULFID    360    360       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    338    338       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   396 AA;  44646 MW;  5FE23A0AC7F91572 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 396;
  Best Local Similarity   54.3%;  Pred. No. 8.8e-30;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        282 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 341

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:||||| ||||
Db        342 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 396


RESULT 12
BMP2_HUMAN
ID   BMP2_HUMAN     STANDARD;      PRT;   396 AA.
AC   P12643;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN   BMP2 OR BMP2A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89072730; PubMed=3201241;
RA   Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
RA   Kriz R.W., Hewick R.M., Wang E.A.;
RT   "Novel regulators of bone formation: molecular clones and
RT   activities.";
RL   Science 242:1528-1534(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.;
RT   "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
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RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.
RX   MEDLINE=99175323; PubMed=10074410;
RA   Scheufler C., Sebald W., Huelsmeyer M.;
RT   "Crystal structure of human bone morphogenetic protein-2 at 2.7 A
RT   resolution.";
RL   J. Mol. Biol. 287:103-115(1999).
CC   -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND
CC       COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
CC       LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
CC       SMALL INTESTINE.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M22489; AAA51834.1; -.
DR   EMBL; AF040249; AAF21646.1; -.
DR   EMBL; AL035668; CAB82007.1; -.
DR   PIR; B37278; BMHU2.
DR   PDB; 3BMP; 12-MAR-00.
DR   PDB; 1ES7; 07-OCT-00.
DR   Genew; HGNC:1069; BMP2.
DR   MIM; 112261; -.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
KW   3D-structure.
FT   SIGNAL       1     23       POTENTIAL.
FT   PROPEP      24    282
FT   CHAIN      283    396       BONE MORPHOGENETIC PROTEIN 2.
FT   DISULFID   296    361
FT   DISULFID   325    393
FT   DISULFID   329    395
FT   DISULFID   360    360       INTERCHAIN.
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   STRAND     295    295
FT   STRAND     297    299
FT   STRAND     302    304
FT   TURN       305    309
FT   TURN       311    313
FT   STRAND     314    316
FT   STRAND     319    321
FT   STRAND     324    326
FT   STRAND     328    328
FT   TURN       331    332
FT   STRAND     339    339
FT   HELIX      341    352
FT   TURN       354    355
FT   STRAND     361    374
FT   TURN       376    377
FT   STRAND     380    396
SQ   SEQUENCE   396 AA;  44702 MW;  20653A3987B25E60 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 396;
  Best Local Similarity   54.3%;  Pred. No. 8.8e-30;
  Matches   63;  Conservative   17;  Mismatches   34;  Indels    2;  Gaps    2;

Qy          5 RQGK-RPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              || | :  | ||: | |  |:|:| |:||:|||:||  | ||:| | | |||  ||  ||
Db        282 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 341

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||::|||:||::    |   |||| || ||:|::|    || | |:|||| ||||
Db        342 HAIVQTLVNSVN-SKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 396


RESULT 13
BMP4_XENLA
ID   BMP4_XENLA     STANDARD;      PRT;   401 AA.
AC   P30885;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 4 precursor (BMP-4).
GN   BMP-4 OR DVR-4.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92378616; PubMed=1510675;
RA   Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT   "Genes for bone morphogenetic proteins are differentially transcribed
RT   in early amphibian embryos.";
RL   Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=93048825; PubMed=1425343;
RA   Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hogan B.L.;
RT   "DVR-4 (bone morphogenetic protein-4) as a posterior-ventralizing
RT   factor in Xenopus mesoderm induction.";
RL   Development 115:639-647(1992).
CC   -!- FUNCTION: POSTERIOR-VENTRALIZING FACTOR IN XENOPUS MESODERM
CC       INDUCTION. INDUCES POSTEROVENTRAL MESODERM AND COUNTERACTS
CC       DORSALIZING SIGNALS SUCH AS ACTIVIN.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X63426; CAA45020.1; -.
```

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DR   PIR; JH0689; JH0689.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20    287       BY SIMILARITY.
FT   CHAIN       288    401       BONE MORPHOGENETIC PROTEIN 4.
FT   DISULFID    301    366       BY SIMILARITY.
FT   DISULFID    330    398       BY SIMILARITY.
FT   DISULFID    334    400       BY SIMILARITY.
FT   DISULFID    365    365       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    204    204       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    343    343       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    358    358       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   401 AA;  45988 MW;  3580DEC4B9890047 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 401;
  Best Local Similarity   52.1%;  Pred. No. 8.9e-30;
  Matches   63;  Conservative   21;  Mismatches   31;  Indels    6;  Gaps    2;

Qy          4 TRQGKRPSKNLKAR-----CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH 58
              ||: ||  |  : |      | | :|:|:| |:||:|||:||  |:||:| | | |||  |
Db        282 TRRSKRSPKQQRPRKKNKHCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADH 341

Qy         59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGC 118
              |  ||||::|||:||::  | |   |||| || ||:|::|  : || | |::|||| |||
Db        342 LNSTNHAIVQTLVNSVN-SSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC 400

Qy        119 R 119
              |
Db        401 R 401


RESULT 14
DECA_DROSI
ID   DECA_DROSI     STANDARD;      PRT;   593 AA.
AC   P91706;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Decapentaplegic protein precursor (DPP-C protein).
GN   DPP.
OS   Drosophila simulans (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7240;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NET DP1;
RX   MEDLINE=97225212; PubMed=9071585;
RA   Newfeld S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA   de Cuevas M., Gelbart W.M.;
RT   "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL   Genetics 145:297-309(1997).
CC   -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC       TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC       DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC       EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC       VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC       TOGETHER WITH SCW (BY SIMILARITY).
CC   -!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC       HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC       ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED
CC       WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
CC       AND MIDGUT MESODERM (BY SIMILARITY).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U63854; AAC47554.1; -.
DR   HSSP; P12643; 3BMP.
DR   FlyBase; FBgn0015673; Dsim\dpp.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW   Signal.
FT   SIGNAL        1     15       POTENTIAL.
FT   PROPEP       16    461       BY SIMILARITY.
FT   CHAIN       462    593       DECAPENTAPLEGIC PROTEIN.
FT   DISULFID    492    558       BY SIMILARITY.
FT   DISULFID    521    590       BY SIMILARITY.
FT   DISULFID    525    592       BY SIMILARITY.
FT   DISULFID    557    557       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    347    347       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    382    382       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    534    534       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   593 AA;  66248 MW;  F0BDB21209F44380 CRC64;

  Query Match             53.5%;  Score 347;  DB 1;  Length 593;
  Best Local Similarity   49.6%;  Pred. No. 1.4e-29;
  Matches   58;  Conservative   24;  Mismatches   33;  Indels    2;  Gaps    1;

Qy          5 RQGKRPS--KNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              || :|:  ||     | | :|:|:| |:||||||:||| |:|::| | | |||  |    |
Db        477 RQPRRPTRRKNHDDTCRRHSLYVDFSDVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST 536

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:|||:|:|:|   |   ||||:|  :::|:::  : || | |::| |  ||||
Db        537 NHAVVQTLVNNMNPGKVPKACCVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVGCGCR 593


RESULT 15
BMP4_CHICK
ID   BMP4_CHICK     STANDARD;      PRT;   405 AA.
AC   Q90752;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Bone morphogenetic protein 4 precursor (BMP-4).
GN   BMP4 OR BMP-4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=White leghorn;
RX   MEDLINE=94163974; PubMed=8119128;
RA   Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT   "Bone morphogenetic proteins and a signalling pathway that controls
RT   patterning in the developing chick limb.";
RL   Development 120:209-218(1994).
RN   [2]
```

```
RP   FUNCTION.
RX   MEDLINE=99128179; PubMed=9927590;
RA   Pizette S., Niswander L.;
RT   "BMPs negatively regulate structure and function of the limb apical
RT   ectodermal ridge.";
RL   Development 126:883-894(1999).
CC   -!- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE
CC       LIMB APICAL ECTODERMAL RIDGE.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X75915; CAA53514.1; -.
DR   PIR; I50608; I50608.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20    291       BY SIMILARITY.
FT   CHAIN       292    405       BONE MORPHOGENETIC PROTEIN 4.
FT   DISULFID    305    370       BY SIMILARITY.
FT   DISULFID    334    402       BY SIMILARITY.
FT   DISULFID    338    404       BY SIMILARITY.
FT   DISULFID    369    369       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    208    208       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    347    347       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    362    362       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   405 AA;  46057 MW;  544302DBA0A40F81 CRC64;

  Query Match             53.3%;  Score 346;  DB 1;  Length 405;
  Best Local Similarity   52.1%;  Pred. No. 1.2e-29;
  Matches   63;  Conservative   21;  Mismatches   31;  Indels    6;  Gaps    2;

Qy          4 TRQGKRP-----SKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSH 58
              ||: :|      |:  |  | | ||:|:| |:||:|||:||  |:||:| | | |||  |
Db        286 TRRARRSPKHHGSRKNKKNCRRHALYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADH 345

Qy         59 LEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGC 118
              |  ||||::|||:||::  | |   ||||  || ||:|::|  : || | |::|||| |||
Db        346 LNSTNHAIVQTLVNSVN-SSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGC 404

Qy        119 R 119
              |
Db        405 R 405


Search completed: February 18, 2004, 17:42:32
Job time : 15 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 17:39:10 ; Search time 35 Seconds
(without alignments)
877.379 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATRQGKRPSKNLKARCSR.....ANNVVYKQYEDMVVESCGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	640	98.6	249	11	Q8BRW9	Q8brw9 mus musculu
2	637	98.2	500	13	Q9W6G0	Q9w6g0 gallus gall
3	587	90.4	324	13	Q9YHW9	Q9yhw9 gallus gall
4	563	86.7	257	13	O42303	O42303 brachydanio
5	534.5	82.4	126	13	O93573	O93573 gallus gall
6	527.5	81.3	261	13	Q9W6C0	Q9w6c0 brachydanio
7	527	81.2	413	13	Q9DGN4	Q9dgn4 xenopus lae
8	524	80.7	399	13	Q9W753	Q9w753 xenopus lae
9	524	80.7	412	13	O12938	O12938 brachydanio
10	491	75.7	294	6	Q9BDW9	Q9bdw9 macaca fasc
11	491	75.7	447	6	Q9BDW8	Q9bdw8 cercopithec
12	386	59.5	441	11	Q99MY1	Q99my1 mus musculu
13	368.5	56.8	361	5	O96504	O96504 branchiosto
14	368	56.7	204	5	Q9XZ69	Q9xz69 tripneustes
15	366	56.4	411	5	Q9U418	Q9u418 branchiosto
16	365	56.2	405	5	Q9U5E8	Q9u5e8 ptychodera
17	361	55.6	289	5	Q9XYQ8	Q9xyq8 strongyloce
18	359	55.3	417	5	Q9XYQ7	Q9xyq7 lytechinus
19	357.5	55.1	509	5	Q8WS99	Q8ws99 archaster t
20	357	55.0	67	11	Q8K4X5	Q8k4x5 rattus norv
21	355.5	54.8	178	5	Q25211	Q25211 junonia coe
22	355.5	54.8	461	5	Q8MXZ3	Q8mxz3 hemicentrot
23	354	54.5	67	6	O02783	O02783 bos taurus
24	350	53.9	277	13	Q90Y82	Q90y82 lampetra ja
25	349.5	53.9	411	13	O57573	O57573 brachydanio
26	349.5	53.9	411	13	O93369	O93369 brachydanio
27	348	53.6	398	13	Q90YD7	Q90yd7 xenopus tro
28	347.5	53.5	128	5	Q95W38	Q95w38 schistocerc
29	347	53.5	588	5	Q9VQC6	Q9vqc6 drosophila
30	346	53.3	400	13	O73818	O73818 xenopus lae
31	346	53.3	400	13	Q91703	Q91703 xenopus lae
32	346	53.3	443	5	O76851	O76851 halocynthia
33	345	53.2	400	13	Q90YD6	Q90yd6 xenopus tro
34	344.5	53.1	411	13	O13108	O13108 brachydanio
35	343	52.9	378	5	Q8MXC2	Q8mxc2 acropora mi
36	342.5	52.8	191	5	Q26468	Q26468 schistocerc
37	342	52.7	373	13	Q98950	Q98950 gallus gall
38	342	52.7	373	13	Q90723	Q90723 gallus gall
39	342	52.7	400	13	O57574	O57574 brachydanio
40	342	52.7	407	5	Q8MWG4	Q8mwg4 patella vul
41	341	52.5	422	5	Q8IAE3	Q8iae3 stichopus j
42	340	52.4	400	13	O13107	O13107 brachydanio
43	340	52.4	403	13	Q8JIK0	Q8jik0 cyprichromi
44	340	52.4	403	13	Q8JIJ7	Q8jij7 julidochrom
45	340	52.4	403	13	Q8JIJ4	Q8jij4 steatocranu

ALIGNMENTS

RESULT 1
Q8BRW9
ID Q8BRW9 PRELIMINARY; PRT; 249 AA.
AC Q8BRW9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Growth differentiation factor 5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK041168; BAC30847.1; -.
FT NON_TER 1 1
SQ SEQUENCE 249 AA; 28409 MW; E6EA047F06B57189 CRC64;

Query Match 98.6%; Score 640; DB 11; Length 249;
Best Local Similarity 98.3%; Pred. No. 1.7e-67;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 190

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        191 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 249
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RESULT 2

```
Q9W6G0
ID   Q9W6G0      PRELIMINARY;      PRT;   500 AA.
AC   Q9W6G0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   GDF-5 protein.
GN   GDF5.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;  .
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99146893; PubMed=10021348;
RA   Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
RA   Ladher R., Allen S., MacPherson S., Luyten F.P., Archer C.W.;
RT   "Mechanisms of GDF-5 action during skeletal development.";
RL   Development 126:1305-1315(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF123389; AAD30451.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   500 AA;  55952 MW;  1DE8385A3119A598 CRC64;

  Query Match             98.2%;  Score 637;  DB 13;  Length 500;
  Best Local Similarity   97.5%;  Pred. No. 8.6e-67;
  Matches  116;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              |||||||||||||| |||||||||||||||||||||||:|||||||||||||||||||||
Db        382 PLATRQGKRPSKNLKPRCSRKALHVNFKDMGWDDWIIAPLEYEAYHCEGLCEFPLRSHLE 441

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        442 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 500


RESULT 3
Q9YHW9
ID   Q9YHW9      PRELIMINARY;      PRT;   324 AA.
AC   Q9YHW9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Growth differentiation factor 5 (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leg bud;
RX   MEDLINE=99119368; PubMed=9918693;
RA   Merino R., Macias D., Ganan Y., Economides A.N., Wang X., Wu Q.,
RA   Stahl N., Sampath K.T., Varona P., Hurle J.M.;
RT   "Expression and function of Gdf-5 during digit skeletogenesis in the
RT   embryonic chick leg bud.";
RL   Dev. Biol. 206:33-45(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF075441; AAD14568.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
FT   NON_TER     324    324
SQ   SEQUENCE   324 AA;  37206 MW;  0B8A7CB111375007 CRC64;

  Query Match             90.4%;  Score 587;  DB 13;  Length 324;
  Best Local Similarity   97.3%;  Pred. No. 4.3e-61;
  Matches  107;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        215 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAYHCEGLCEFPLRSHLE 274

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYED 110
              |||||||||||||||||||| ||||||||||||||||||||||||||||:
Db        275 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEE 324


RESULT 4
O42303
ID   O42303      PRELIMINARY;      PRT;   257 AA.
AC   O42303;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Contact (Fragment).
GN   GDF5.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97398455; PubMed=9256353;
RA   Bruneau S., Mourrain P., Rosa F.M.;
RT   "Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT   cell lineages in the developing pectoral fins and head and is
RT   regulated by retinoic acid.";
RL   Mech. Dev. 65:163-173(1997).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; Y12005; CAA72733.1; -.
DR   HSSP; P12643; 3BMP.
DR   ZFIN; ZDB-GENE-990415-39; gdf5.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
FT   CHAIN       140    257       POTENTIAL.
SQ   SEQUENCE   257 AA;  29787 MW;  6D64F0542F948849 CRC64;

  Query Match             86.7%;  Score 563;  DB 13;  Length 257;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-58;
  Matches   98;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          6 QGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHA 65
              :||:| || | ||:|| |||||:|||||||||||||||||:|:|:||:||||||||||
Db        144 RGKKPIKNPKQRCNRKQLHVNFKEMGWDDWIIAPLEYEAFHCDGVCDFPIRSHLEPTNHA 203
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Qy          66 VIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
               :|||||||||| ||||| ||||||||||||:||||||||||||||||||||||
Db         204 IIQTLMNSMDPRSTPPTCCVPTRLSPISILYIDSANNVVYKQYEDMVVESCGCR 257


RESULT 5
O93573
ID   O93573      PRELIMINARY;      PRT;   126 AA.
AC   O93573;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Putative growth/differentiation factor 6/7 (Fragment).
GN   GDF6/7.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99026113; PubMed=9808626;
RA   Lee K.J., Mendelsohn M., Jessell T.M.;
RT   "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT   of a discrete class of commissural interneurons in the mouse spinal
RT   cord.";
RL   Genes Dev. 12:3394-3407(1998).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF089086; AAC97113.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   126 AA;  14265 MW;  CB824D280F44A394 CRC64;

  Query Match             82.4%;  Score 534.5;  DB 13;  Length 126;
  Best Local Similarity   79.0%;  Pred. No. 2.4e-55;
  Matches   94;  Conservative   13;  Mismatches   11;  Indels    1;  Gaps    1;

Qy           2 LATRQGKR-PSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
               :| | | |   | | ||||| ||||||::||||||||:|||:||||:|:||||||||
Db           8 IAARSGGRGHGKKAKTRCSRKPLHVNFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLE 67

Qy          61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
               |||||:|||||||||||||||: |||::|||||||:||| ||||||||||||||:||||
Db          68 PTNHAIIQTLMNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVETCGCR 126


RESULT 6
Q9W6C0
ID   Q9W6C0      PRELIMINARY;      PRT;   261 AA.
AC   Q9W6C0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Growth/differentiation factor 7 (Fragment).
GN   GDF7.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99148135; PubMed=10022976;
RA   Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
RA   Foernzler D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT   "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT   belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the
RT   TGF-beta superfamily.";
RL   Genome Res. 9:121-129(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF113023; AAD20829.1; -.
DR   HSSP; P12643; 3BMP.
DR   ZFIN; ZDB-GENE-990714-1; gdf7.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   261 AA;  29414 MW;  77346E977036A104 CRC64;

  Query Match             81.3%;  Score 527.5;  DB 13;  Length 261;
  Best Local Similarity   76.0%;  Pred. No. 3.7e-54;
  Matches   95;  Conservative   11;  Mismatches   12;  Indels    7;  Gaps    1;

Qy           2 LATRQGKRP-------SKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFP 54
               || | | |         : ||||| |||||::||||||||||:|||:||||||:||
Db         137 LAGRPGVGPITSGGKGGGRRRTRCSRKPLHVNFKELGWDDWIIAPLDYEAYHCEGLCDFP 196

Qy          55 LRSHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVE 114
               |||||||||||:|||||||||||||||: |||::|||||||:||| ||||||||||||||
Db         197 LRSHLEPTNHAIIQTLMNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVE 256

Qy         115 SCGCR 119
               |||||
Db         257 SCGCR 261


RESULT 7
Q9DGN4
ID   Q9DGN4      PRELIMINARY;      PRT;   413 AA.
AC   Q9DGN4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Growth/differentiation factor 16 precursor protein.
GN   GDF16.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20368184; PubMed=10906478;
RA   Vokes S.A., Krieg P.A.;
RT   "Gdf16, a novel member of the growth/differentiation factor subgroup
RT   of the TGF-beta superfamily, is expressed in the hindbrain and
RT   epibranchial placodes.";
RL   Mech. Dev. 95:279-282(2000).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF239676; AAF99597.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
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KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   413 AA;  46510 MW;  5F1B0D7D97E591F6 CRC64;

  Query Match             81.2%;  Score 527;  DB 13;  Length 413;
  Best Local Similarity   77.3%;  Pred. No. 7.3e-54;
  Matches   92;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              |  |  ||  :|  | |||:| | ||||::|||||||||:|||:||||:|:|||||||
Db        295 PTRTNNGKGHAKKSKTRCSKKPLLVNFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLE 354

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||:|||||||||||||||: |||::|||||||:||| ||||||||||||||| ||
Db        355 PTNHAIIQTLMNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVESCSCR 413


RESULT 8
Q9W753
ID   Q9W753      PRELIMINARY;      PRT;   399 AA.
AC   Q9W753;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Growth and differentiation factor 6.
GN   GDF6.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99396700; PubMed=10393114;
RA   Chang C., Hemmati-Brivanlou A.;
RT   "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL   Development 126:3347-3357(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF155125; AAD38402.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   399 AA;  45571 MW;  C549D973B50B8517 CRC64;

  Query Match             80.7%;  Score 524;  DB 13;  Length 399;
  Best Local Similarity   77.6%;  Pred. No. 1.6e-53;
  Matches   90;  Conservative   15;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 TRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTN 63
              :| |||  :  : |||:| ||||||::|||||||||||||| ||||:|:||||||||||
Db        284 SRHGKRHGRKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAHHCEGVCDFPLRSHLEPTN 343

Qy         64 HAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||:|||||||:| |||| |||:|:|||||:||: |||||||||||||||||
Db        344 HAIIQTLMNSMNPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 399


RESULT 9
O12938
ID   O12938      PRELIMINARY;      PRT;   412 AA.
AC   O12938;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Dynamo protein precursor.
GN   GDF6A OR DYNAMO.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97231294; PubMed=9076689;
RA   Bruneau S., Rosa F.;
RT   "Dynamo a new Zebrafish DVR member of the TGF-B superfamily is
RT   expressed in the posterior neural tube and is up regulated by Sonic
RT   hedgehog.";
RL   Mech. Dev. 61:199-212(1997).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; X99769; CAA68102.1; -.
DR   HSSP; P12643; 3BMP.
DR   ZFIN; ZDB-GENE-980526-442; gdf6a.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN       293    412       DYNAMO PROTEIN.
SQ   SEQUENCE   412 AA;  47072 MW;  4076E262C4481121 CRC64;

  Query Match             80.7%;  Score 524;  DB 13;  Length 412;
  Best Local Similarity   74.6%;  Pred. No. 1.6e-53;
  Matches   88;  Conservative   18;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 LATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEP 61
              |  | |||  |  |:|||:| |||||:::|||||:||||:|||:|||||:|:|||||||
Db        295 LPNRHGKRHGKKSKSRCSKKPLHVNFRELGWDDWVIAPLDYEAYHCEGMCDFPLRSHLEP 354

Qy         62 TNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:||||||||:| : ||: |||::|||||||:||: |||||||||||||||||||
Db        355 TNHAIIQTLMNSMNPSNMPPSCCVPSKLSPISILYIDAGNNVVYKQYEDMVVESCGCR 412


RESULT 10
Q9BDW9
ID   Q9BDW9      PRELIMINARY;      PRT;   294 AA.
AC   Q9BDW9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Growth/differentiation factor 7 (Fragment).
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebral cortex motor area;
RX   MEDLINE=21136583; PubMed=11238730;
RA   Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RT   "Growth/differentiation factor 7 is preferentially expressed in the
RT   primary motor area of the monkey neocortex.";
RL   J. Neurochem. 76:1455-1464(2001).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF254567; AAK27794.1; -.
DR   HSSP; P12643; 3BMP.
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DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   294 AA;  31792 MW;  49B7BCD9F27AF39F CRC64;

  Query Match             75.7%;  Score 491;  DB 6;  Length 294;
  Best Local Similarity   73.5%;  Pred. No. 9e-50;
  Matches   83;  Conservative   19;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
              |:   :  ::|||||:|||:||::||||||||||:|||:||||:|:||||||||||||:
Db        182 GRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 241

Qy         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:|||:|:: | : ||| ||||||||:||:||||||||||||:||||
Db        242 IQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR 294


RESULT 11
Q9BDW8
ID   Q9BDW8      PRELIMINARY;      PRT;   447 AA.
AC   Q9BDW8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Growth/differentiation factor 7.
GN   GDF7.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21136583; PubMed=11238730;
RA   Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RT   "Growth/differentiation factor 7 is preferentially expressed in the
RT   primary motor area of the monkey neocortex.";
RL   J. Neurochem. 76:1455-1464(2001).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF254569; AAK30842.1; -.
DR   EMBL; AF254568; AAK30842.1; JOINED.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   447 AA;  46866 MW;  DF46D591925A8391 CRC64;

  Query Match             75.7%;  Score 491;  DB 6;  Length 447;
  Best Local Similarity   73.5%;  Pred. No. 1.5e-49;
  Matches   83;  Conservative   19;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
              |:   :  ::|||||:|||:||::||||||||||:|||:||||:|:||||||||||||:
Db        335 GRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 394

Qy         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||:|||:|:: | : ||| ||||||||:||:||||||||||||:||||
Db        395 IQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR 447


RESULT 12
Q99MY1
ID   Q99MY1      PRELIMINARY;      PRT;   441 AA.
AC   Q99MY1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Growth/differentiation factor 7 (Fragment).
GN   GDF7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TT2;
RX   MEDLINE=21136583; PubMed=11238730;
RA   Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RT   "Growth/differentiation factor 7 is preferentially expressed in the
RT   primary motor area of the monkey neocortex.";
RL   J. Neurochem. 76:1455-1464(2001).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF254571; AAK30843.1; -.
DR   EMBL; AF254570; AAK30843.1; JOINED.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER     441     441
SQ   SEQUENCE   441 AA;  45617 MW;  74DA312A853701F0 CRC64;

  Query Match             59.5%;  Score 386;  DB 11;  Length 441;
  Best Local Similarity   68.8%;  Pred. No. 3.9e-37;
  Matches   64;  Conservative   19;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          7 GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAV 66
              |:   :  ::|||||:|||:||::||||||||||:|||:||||:|:||||||||||||:
Db        349 GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 408

Qy         67 IQTLMNSMDPESTPPTACVPTRLSPISILFIDS 99
              ||||:|||:|:: | : ||| |||||||||:||:
Db        409 IQTLLNSMAPDAAPASCCVPARLSPISILYIDA 441


RESULT 13
O96504
ID   O96504      PRELIMINARY;      PRT;   361 AA.
AC   O96504;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 2/4.
GN   AMPHIBMP2/4.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98401944; PubMed=9733108;
RA   Panopoulou G.D., Clark M.D., Holland L.Z., Lehrach H., Holland N.D.;
RT   "AmphiBMP2/4, an amphioxus bone morphogenetic protein closely related
RT   to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
RT   into evolution of dorsoventral axis specification.";
RL   Dev. Dyn. 213:130-139(1998).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF068750; AAC97488.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
```

```
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   361 AA;  41517 MW;  09FF5FE6C9785DD1 CRC64;

  Query Match           56.8%;  Score 368.5;  DB 5;  Length 361;
  Best Local Similarity  52.0%;  Pred. No. 3.6e-35;
  Matches   64;  Conservative   25;  Mismatches   29;  Indels    5;  Gaps    1;

Qy          2 LATRQ-----GKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLR 56
              :|:||     |:  : ||| | | :|:|:| |:||:|||:||  |:|::| | | |||
Db        239 VASRQKRANGRKKQRRRLKANCRRHSLYVDFSDVGWNDWIVAPPGYQAYYCHGECPFPLA 298

Qy         57 SHLEPTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESC 116
               ||  ||||::|||:||::| : |   |||| ||||:|::: : || | |:||||| |
Db        299 DHLNSTNHAIVQTLVNSVNPLAVPKACCVPTDLSPISMLYLNENDQVVLKNYQDMVVEGC 358

Qy        117 GCR 119
              |||
Db        359 GCR 361


RESULT 14
Q9XZ69
ID   Q9XZ69      PRELIMINARY;      PRT;   204 AA.
AC   Q9XZ69;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 2/4 homolog (Fragment).
GN   BMP2/4.
OS   Tripneustes gratilla (Hawaian sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
OC   Tripneustes.
OX   NCBI_TaxID=7673;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99262121; PubMed=10329409;
RA   Hwang S.L., Chen C.A., Chen C.;
RT   "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RT   closely related to vertebrate BMP2 and BMP4 with maximal expression at
RT   the later stages of embryonic development.";
RL   Biochem. Biophys. Res. Commun. 258:457-463(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF133305; AAD30538.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   204 AA;  23697 MW;  CE829BDC2AA9F077 CRC64;

  Query Match           56.7%;  Score 368;  DB 5;  Length 204;
  Best Local Similarity  53.8%;  Pred. No. 2.2e-35;
  Matches   63;  Conservative   19;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              ::|  ||  | ||| | |  |:|:| |: |:|||:||  |:|::| | | ||| |  |
Db         88 SSRSRKRKGKRLKANCRRHPLYVDFSDVHWNDWIVAPAGYQAYYCHGECPFPLAEHLNTT 147

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||::|||:||::|   |   |||| || ||:|::|    ||. | |:||||| ||||
Db        148 NHAIVQTLVNSVNPALVPKACCVPTELSAISMLYLDEYEKVVLKNYQDMVVEGCGCR 204


RESULT 15
Q9U418
ID   Q9U418      PRELIMINARY;      PRT;   411 AA.
AC   Q9U418;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 2/4.
GN   BMP2/4.
OS   Branchiostoma belcheri (Amphoxius).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7741;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yasui K., Saiga H., Uemura M., Semba I.;
RT   "Early body formation and expression pattern of genes encoding
RT   secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF206325; AAF19841.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   411 AA;  46929 MW;  F579898060F18355 CRC64;

  Query Match           56.4%;  Score 366;  DB 5;  Length 411;
  Best Local Similarity  53.0%;  Pred. No. 8.3e-35;
  Matches   62;  Conservative   23;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          3 ATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPT 62
              |  : |   : ||| | | :|:|:| |:||:|||:||  |:|::| | | ||| ||  |
Db        295 ANGRKKHQRRRLKANCRRHSLYVDFSDVGWNDWIVAPPGYQAYYCHGECPFPLADHLNST 354

Qy         63 NHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||::|||:||::| : |   |||| |||||:|:::  : || | |:||||| ||||
Db        355 NHAIVQTLVNSVNPLAVPKACCVPTDLSPISMLYLNENDQVVLKNYQDMVVEGCGCR 411


Search completed: February 18, 2004, 17:43:20
Job time : 36 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 17:36:44 ; Search time 40 Seconds
(without alignments)
472.212 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATRQGKRPSKNLKARCSR.....ANNVVYKQYEDMVVESCGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	649	100.0	119	21	AAY44296	Mutant human MP52
2	645	99.4	119	17	AAW06920	Human MP52 growth
3	645	99.4	119	18	AAW19846	Human bone inducin
4	645	99.4	120	16	AAR78731	Murine protein MP5
5	645	99.4	120	18	AAW26590	Human MP52 protein
6	645	99.4	120	22	AAE10973	Human MP-52 protei
7	645	99.4	120	24	ABG73290	Amino acid sequenc
8	645	99.4	401	14	AAR40800	TGF-beta-like clon
9	645	99.4	501	16	AAR69600	New TGF-beta famil
10	645	99.4	501	18	AAW36100	Human MP52. Homo
11	645	99.4	501	18	AAW19210	Human TGF-beta pro
12	645	99.4	501	18	AAW11900	Human high mol. wt
13	645	99.4	501	18	AAW01799	Human MP52 protein
14	645	99.4	501	18	AAW12770	Human bone morphog
15	645	99.4	501	19	AAW44868	TGF-beta superfami
16	645	99.4	501	19	AAW33008	Human MP52. Homo
17	645	99.4	501	22	AAB70529	Human TGF-beta MP5
18	640	98.6	495	15	AAR60022	Growth differentia
19	640	98.6	495	22	AAB84550	Amino acid sequenc
20	640	98.6	495	24	ABG76018	Mouse growth diffe
21	639	98.5	119	21	AAY70752	Wild type mature h
22	639	98.5	119	21	AAY70756	Methionine oxidise
23	639	98.5	119	21	AAY70757	Methionine alkylat
24	639	98.5	119	21	AAY70758	Tryptophan allylsu
25	639	98.5	120	23	AAM51932	Human TGFbeta prot
26	639	98.5	501	17	AAR95635	Cartilage-derived
27	639	98.5	501	21	AAY92034	Human growth diffe
28	559	86.1	102	21	AAB09553	Human CDMP-1/GDF-5
29	559	86.1	102	21	AAB02819	Human CDMP-1/GDF-5
30	559	86.1	102	21	AAY92578	CDMP-1/GDF-5 finge
31	543	83.7	120	23	AAM51933	Murine TGFbeta pro
32	543	83.7	125	24	ABG76037	Human GDF-6 C-term
33	543	83.7	134	16	AAR66867	GDF-6. Mus sp. A
34	543	83.7	134	21	AAB12986	Murine growth diff
35	543	83.7	263	16	AAR78739	Murine mV2 protein
36	543	83.7	263	18	AAW26595	Murine BMP-13 homo
37	540	83.2	321	16	AAR78730	Human mature VL-1
38	540	83.2	321	18	AAW26591	Human bone morphog
39	540	83.2	321	22	AAE10982	Human full length
40	540	83.2	321	24	ABG73298	Human bone morphog
41	540	83.2	455	22	AAM50216	Human growth/diffe
42	540	83.2	455	23	AAU79173	Human growth/diffe
43	540	83.2	455	23	AAE17604	Human extracellula
44	538	82.9	263	22	AAE10985	Murine partial mV2
45	538	82.9	263	24	ABG73301	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAY44296
ID AAY44296 standard; Protein; 119 AA.
XX
AC AAY44296;
XX
DT 29-FEB-2000 (first entry)
XX
DE Mutant human MP52 monomer protein.
XX
KW Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta;
KW pKOT279 expression vector; osteocyte; bone morphogenetic; osteopathic;
KW anti-arthritic activity; cartilage; osteoporosis; osteoarthritis;
KW arthrosteitis; fracture; achondroplasia; dyschondrogenesis;
KW achondrogenesis; palatoschisis; dysosteogenesis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 83
FT /note= "Wild-type Cys replaced by Ala"
XX
PN WO9961611-A1.
XX
PD 02-DEC-1999.
XX
PF 14-MAY-1999; 99WO-IB00866.
XX
PR 22-MAY-1998; 98JP-0141379.
XX
PA (HMRI) HOECHST MARION ROUSSEL LTD.

XX
PI Kawai S, Kimura M, Muraki Y, Katsuura M;
XX
DR WPI; 2000-097122/08.
DR N-PSDB; AAZ29328.
XX
PT Novel monomer protein used for prevention and treatment of bone and/or
PT cartilage diseases -
XX
PS Claim 4; Page 20; 26pp; English.
XX
CC The present sequence is a mutant human MP52 monomer protein, which
CC belongs to transforming growth factor-beta (TGF-beta)
CC superfamily. Mutant MP52 can be produced in E. coli cells by
CC transforming them with pKOT279 expression vector containing a mutated
CC MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is
CC capable of inducing differentiation in osteocytes and exhibits bone
CC morphogenetic, osteopathic and anti-arthritic activity. The MP52 monomer
CC protein is used for prevention and treatment of cartilage and/or bone
CC diseases such as osteoporosis, osteoarthritis, arthrosteitis, damage of
CC cartilage, regeneration of bone, cartilage deficit caused by injury and
CC tumour dissection, fracture, congenital bone and/or cartilage diseases
CC such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis
CC and dysosteogenesis and a deficit of root of teeth and a tooth socket.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 649; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
Db 1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy 61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
Db 61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119

RESULT 2
AAW06920
ID AAW06920 standard; Protein; 119 AA.
XX
AC AAW06920;
XX
DT 27-JUN-1997 (first entry)
XX
DE Human MP52 growth factor residues 383-501.
XX
KW Human; MP52; growth factor; monomer; dimer; treatment; bone;
KW cartilage; dental; disorder; fracture; bone loss;
KW periodontal disease; calcification; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO9633215-A1.
XX
PD 24-OCT-1996.
XX
PF 19-APR-1996; 96WO-JP01062.
XX
PR 17-NOV-1995; 95JP-0322403.
PR 19-APR-1995; 95JP-0093664.
XX
PA (FARH) HOECHST JAPAN LTD.
XX
PI Enomoto K, Katsuura M, Kawai S, Kimura M, Makishima F;
PI Matsumoto T, Mikih, Satoh Y, Takamatsu H;
XX
DR WPI; 1996-485730/48.
DR N-PSDB; AAT46150.
XX
PT Peptide consisting of part of human MP52 growth factor, and its
PT dimer - is used for treatment of bone, cartilage and dental
PT disorders
XX
PS Claim 1; Pages 18-19; 33pp; Japanese.
XX
CC The present sequence is residues 383 to 501 of the human MP52
CC growth factor, a dimer of which can be used to treat bone,
CC cartilage and dental disorders, including fractures, bone loss and
CC periodontal disease. The dimer was prepared by transforming a host
CC (preferably E. coli) with a suitable (plasmid) expression vector
CC containing DNA encoding the monomer. The host was cultured, and
CC inclusion bodies from the cells worked up to give the monomer,
CC which was then converted into the dimer. The product was mixed with
CC type 1 pig tendon collagen and injected into the large thigh vein
CC of ICR mice. After 20 days 4 of 4 mice injected with 10 microg of
CC the dimer showed bone/cartilage calcification around the injection
CC site, compared to none in 0 of 4 mice treated with collagen only.
XX
SQ Sequence 119 AA;

Query Match 99.4%; Score 645; DB 17; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.8e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
Db 1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy 61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
Db 61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119

RESULT 3
AAW19846
ID AAW19846 standard; Protein; 119 AA.
XX
AC AAW19846;
XX
DT 12-FEB-1998 (first entry)
XX
DE Human bone inducing factor MP52.
XX
KW Human; bone inducing factor; MP52; collagen; fracture;
KW polyoxyethylene-polyoxypropylene glycol.
XX
OS Homo sapiens.
XX
PN WO9718829-A1.
XX
PD 29-MAY-1997.
XX
PF 14-NOV-1996; 96WO-JP03333.
XX
PR 17-NOV-1995; 95JP-0322402.
XX
PA (FARH) HOECHST JAPAN LTD.
PA (FARH) HOECHST PHARM & CHEM KK.
XX
PI Shimura T, Toriyama S;
XX
DR WPI; 1997-310243/28.
DR N-PSDB; AAT70296.
XX
PT Material for repairing bone and collagen, especially bone fracture
PT or loss - comprising bone-inducing factor and
PT polyoxyethylene-polyoxypropylene glycol compounds
XX
PS Example 4; Page 16-17; 31pp; Japanese.
XX
CC Bone and collagen inducing material has been developed which comprises
CC bone inducing factor and polyoxyethylene-polyoxypropylene glycol

```
CC   compounds. The present sequence represents human bone inducing factor
CC   MP52. This material allows treatment without surgery. It is highly
CC   absorbable because a carrier is used with the bone inducing factor,
CC   and undergoes reversible sol-gel transition depending on the
CC   temperature.
XX
SQ   Sequence   119 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 119;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-59;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 4
AAR78731
ID   AAR78731 standard; Protein; 120 AA.
XX
AC   AAR78731;
XX
DT   25-MAR-2003  (updated)
DT   23-NOV-1995  (first entry)
XX
DE   Murine protein MP52.
XX
KW   Bone morphogenetic protein; MP52; tendon; ligament.
XX
OS   Mus musculus.
XX
PN   WO9516035-A2.
XX
PD   15-JUN-1995.
XX
PF   06-DEC-1994;   94WO-US14030.
XX
PR   02-NOV-1994;   94US-0333576.
PR   07-DEC-1993;   93US-0164103.
PR   25-MAR-1994;   94US-0217780.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Celeste AJ,  Melton DA,  Rosen VA,  Thomsen GH,  Wolfman NM;
PI    Wozney JM;
XX
DR   WPI; 1995-224320/29.
DR   N-PSDB; AAQ96209.
XX
PT   Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
PT   compsn. for inducing tendon/ligament-like tissue formation
XX
PS   Example; Page 51-52; 84pp; English.
XX
CC   Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
CC   amplification of a 275 bp DNA probe, the internal 269 bp of which
CC   corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding
CC   plasmid subclone PCR1-1#2. This probe was radioactively labelled
CC   and used to screen a murine genomic library. DNA sequence analysis
CC   of one of positively hybridising recombinants named MVR23 indicates
CC   that it encodes a portion of the mouse gene corresp. to the PCR
CC   product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78731).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   120 AA;

  Query Match             99.4%;  Score 645;  DB 16;  Length 120;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-59;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 5
AAW26590
ID   AAW26590 standard; Protein; 120 AA.
XX
AC   AAW26590;
XX
DT   25-MAR-2003  (updated)
DT   21-JAN-1998  (first entry)
XX
DE   Human MP52 protein.
XX
KW   MP52; BMP; bone morphogenetic protein; human; tendon; ligament;
KW   wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
KW   therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..120
FT                   /note= "Claim 5"
FT   Protein         19..120
FT                   /note= "Claim 5"
XX
PN   US5658882-A.
XX
PD   19-AUG-1997.
XX
PF   22-DEC-1994;   94US-0362670.
XX
PR   22-DEC-1994;   94US-0362670.
PR   07-DEC-1993;   93US-0164103.
PR   25-MAR-1994;   94US-0217780.
PR   02-NOV-1994;   94US-0333576.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Celeste AJ,  Melton DA,  Rosen VA,  Thomsen GH,  Wolfman NM;
PI   Wozney JM;
XX
DR   WPI; 1997-424270/39.
XX
PT   Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
PT   - useful for tissue healing and repair, treatment of tendonitis,
PT   improving fixation of tendons to bone etc
XX
PS   Claim 5; Column 39-40; 43pp; English.
XX
CC   This polypeptide comprises human MP52.  A claimed method for
CC   inducing formation of tendon and/or ligament tissues involves the
CC   administration of a composition containing at least one protein
CC   selected from MP52, BMP-12 (see AAW26589) and BMP-13 (see AAW26591).
CC   The method is used for tissue (including skin) healing and repair.
CC   This is useful for treating tendonitis, carpal tunnel syndrome and
CC   other defects of traumatic or congenital origin, in cosmetic
CC   surgery and to improve fixation of tendons or ligaments to bone.
CC   The specified proteins can also be used to increase activity of other
CC   BMPs e.g. BMP-2 (see AAW26597).
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence   120 AA;
```

```
  Query Match           99.4%;  Score 645;  DB 18;  Length 120;
  Best Local Similarity  99.2%;  Pred. No. 1.8e-59;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 6
AAE10973
ID   AAE10973 standard; Protein; 120 AA.
XX
AC   AAE10973;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human MP-52 protein.
XX
KW   Human; MP-52; vulnerary; antiinflammatory; analgesic; ligament defect;
KW   transforming growth factor-beta; TGF-beta; tissue formation; tendonitis;
KW   wound healing; tissue repair; carpal tunnel syndrome; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US6284872-B1.
XX
PD   04-SEP-2001.
XX
PF   28-FEB-1997;   97US-0808324.
XX
PR   22-DEC-1994;   94US-0362670.
PR   07-DEC-1993;   93US-0164103.
PR   25-MAR-1994;   94US-0217780.
PR   02-NOV-1994;   94US-0333576.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Celeste AJ,  Wozney JM,  Rosen VA,  Wolfman NM,  Thomsen GH;
PI   Melton DA;
XX
DR   WPI; 2001-588978/66.
DR   N-PSDB; AAD18317.
XX
PT   New chimeric DNAs, useful for treating tendonitis, carpal tunnel
PT   syndrome and other tendon and ligament defects, comprises DNA encoding
PT   propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
PT   BMP-13 or MP52 -
XX
PS   Disclosure; Column 39-40; 42pp; English.
XX
CC   The invention relates to a chimeric DNA comprising a DNA sequence
CC   encoding a propeptide from a member of the transforming growth factor
CC   (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
CC   encoding an amino acid sequence encoding a mature polypeptide consisting
CC   of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
CC   sequences are useful for producing proteins which induce tendon/ligament
CC   like tissue formation, and for isolating and cloning further DNA
CC   sequences encoding BMP-12 related proteins with similar activity. The
CC   proteins are useful for the induction of tendon/ligament-like tissue
CC   formation, wound healing, ligament and other tissue repair, augmenting
CC   the activity of bone morphogenetic proteins, and for treating tendonitis,
CC   carpal tunnel syndrome and other tendon and ligament defects. The
CC   present sequence is human MP-52 protein.
XX
SQ   Sequence   120 AA;
```

```
  Query Match           99.4%;  Score 645;  DB 22;  Length 120;
  Best Local Similarity  99.2%;  Pred. No. 1.8e-59;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 7
ABG73290
ID   ABG73290 standard; Protein; 120 AA.
XX
AC   ABG73290;
XX
DT   30-APR-2003  (first entry)
XX
DE   Amino acid sequence for human MP52.
XX
KW   Human; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
KW   BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
KW   tendon/ligament-like tissue formation; trauma induced tendon defect;
KW   tendon/ligament-like tissue healing; tendon damage; ligament damage;
KW   tendon fixation; ligament fixation; congenital; ligament defect;
KW   cosmetic plastic surgery; vulnerary; MP52.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..120
FT                   /note= "Specifically claimed in Claim 26"
FT   Region          19..120
FT                   /note= "Specifically claimed in Claim 26"
XX
PN   US2002160494-A1.
XX
PD   31-OCT-2002.
XX
PF   31-AUG-2001; 2001US-0945182.
XX
PR   22-DEC-1994;   94US-0362670.
PR   28-FEB-1997;   97US-0808324.
PR   07-DEC-1993;   93US-0164103.
PR   25-MAR-1994;   94US-0217780.
PR   02-NOV-1994;   94US-0333576.
XX
PA   (CELE/) CELESTE A J.
PA   (WOZN/) WOZNEY J M.
PA   (ROSE/) ROSEN V A.
PA   (WOLF/) WOLFMAN N M.
PA   (THOM/) THOMSEN G H.
PA   (MELT/) MELTON D A.
XX
PI   Celeste AJ,  Wozney JM,  Rosen VA,  Wolfman NM,  Thomsen GH;
PI   Melton DA;
XX
DR   WPI; 2003-238228/23.
DR   N-PSDB; ABX11141.
XX
PT   New bone morphogenetic proteins (designated BMP-12) or related
PT   proteins, useful for inducing tendon/ligament-like tissue formation in
PT   a patient, or for tendon/ligament-like tissue healing or repair (e.g.
PT   for treating tendonitis)  -
XX
PS   Claim 26; Page 21; 46pp; English.
XX
CC   The present invention relates to the isolation of human bone
CC   morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein
CC   (designated BMP-13 or VL-1), and the polynucleotide sequences encoding
```

CC them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of
CC proteins. BMP-12 and VL-1 are characterised by their ability to
CC induce the formation of tendon/ligament-like tissue. The BMP-12
CC proteins of the invention are useful for inducing tendon/ligament-like
CC tissue formation in a patient. They are particularly useful for
CC tendon/ligament-like tissue healing and tissue repair, e.g. for
CC treating tendonitis, or other tendon or ligament defects in a patient.
CC The polynucleotide sequences encoding the BMP-12 proteins are useful
CC for inducing tendon/ligament-like tissue formation in a patient, and
CC for tendon/ligament-like tissue healing and tissue repair. The BMP-12
CC polypeptide and polynucleotide sequences may be used for preventing
CC damage to tendon or ligament tissue, to improve fixation of tendon or
CC ligament to bone or other tissues, to repair congenital or trauma
CC induced tendon or ligament defects, and in cosmetic plastic surgery
CC for attachment or repair of tendons or ligaments. The present sequence
CC represents human MP52.
XX
SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 24; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.8e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120
```

RESULT 8
AAR40800
ID AAR40800 standard; Protein; 401 AA.
XX
AC AAR40800;
XX
DT 25-MAR-2003 (updated)
DT 11-FEB-1994 (first entry)
XX
DE TGF-beta-like clone MP-52 protein.
XX
KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
KW bone; cartilage; tooth; wound repair; immunosuppressor;
KW organ transplant; cosmetic surgery; antibody; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9316099-A2.
XX
PD 19-AUG-1993.
XX
PF 12-FEB-1993; 93WO-EP00350.
XX
PR 12-FEB-1992; 92EP-0102324.
XX
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI Hoetten G, Neidhardt H;
XX
DR WPI; 1993-272824/34.
DR N-PSDB; AAQ47709.
XX
PT New transforming growth factor-beta family proteins and DNA -
PT used in tissue and wound repair, in treatment of bone, cartilage
PT and tooth defects, and antibodies for diagnosis
XX
PS Claim 11; Page 19; 29pp; English.
XX
CC The sequences given in AAR40800 and AAR45447 represent frements of
CC embryo and liver derived human transforming growth factor-beta
CC (TGF-beta) respectively. The full length protein may be used in a
CC pharmaceutical composition for the treatment of various bone, cartilage
CC or tooth defects and in tissue and wound repair processes. These
CC proteins may also be used as immunosuppressors in organ transplants and
CC in cosmetic surgery. Antibodies raised against these proteins may be
CC used for diagnostic purposes.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 401 AA;

Query Match 99.4%; Score 645; DB 14; Length 401;
Best Local Similarity 99.2%; Pred. No. 7.8e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 342

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        343 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 401
```

RESULT 9
AAR69600
ID AAR69600 standard; Protein; 501 AA.
XX
AC AAR69600;
XX
DT 25-MAR-2003 (updated)
DT 10-OCT-1995 (first entry)
XX
DE New TGF-beta family member - MP-52 protein sequence.
XX
KW Transforming growth factor-beta family; mitogenic; differentiation;
KW treatment; prevention; disease; bone; cartilage; connective tissue;
KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
KW tissue regeneration; arthritis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 382
FT /label= mature protein
XX
PN WO9504819-A1.
XX
PD 16-FEB-1995.
XX
PF 09-AUG-1994; 94WO-EP02630.
XX
PR 10-AUG-1993; 93DE-4326829.
PR 25-MAY-1994; 94DE-4418222.
PR 09-JUN-1994; 94DE-4420157.
XX
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI Hotten G, Neidhardt H, Paulista M, Hoetten G;
XX
DR WPI; 1995-090897/12.
DR N-PSDB; AAQ83695.
XX
PT New DNA encoding a new member of the TGF beta family - and
PT related vectors, host cells etc., has mitogenic and
PT differentiation inducing activity, e.g. for treating or
PT preventing diseases of bone and cartilage etc.
XX
PS Claim 6; Page 36; 51pp; German.
XX
CC The amino acid sequence of a novel member of the transforming growth
CC factor-beta (TGF-b) family named MP-52. The gene encodes a protein
CC of 501 amino acids (AA). The protein, or at least the mature protein,
CC has mitogenic and/or differentiation inducing properties useful in
CC the treatment or prevention of diseases of bone, cartilage, connective

```
CC   tissue, skin, mucosa, epithelium or dental tissue.  The protein can also
CC   be used for wound healing and tissue regeneration e.g. in osteoporosis
CC   and arthritis.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 16;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1e-58;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 10
AAW36100
ID   AAW36100 standard; Protein; 501 AA.
XX
AC   AAW36100;
XX
DT   08-MAY-1998  (first entry)
XX
DE   Human MP52.
XX
KW   Bone morphogenetic protein; BMP; processing enzyme; MP52;
KW   BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.
XX
OS   Homo sapiens.
XX
PN   WO9741250-A1.
XX
PD   06-NOV-1997.
XX
PF   28-APR-1997;   97WO-JP01474.
XX
PR   30-APR-1996;   96JP-0130618.
XX
PA   (FARH ) HOECHST YAKUHIN KOGYO KK.
PA   (FARH ) HOECHST PHARM & CHEM KK.
XX
PI   Kimura M,  Makishima F,  Takahashi M;
XX
DR   WPI; 1997-549748/50.
DR   N-PSDB; AAT98191.
XX
PT   Production of mature bone morphogenetic protein  - by treatment of
PT   precursor protein with a processing enzyme such as furin either
PT   directly or by expressing them both in the same host
XX
PS   Example 1; Pages 21-25; 34pp; Japanese.
XX
CC   The present sequence is MP52, which is a bone morphogenetic
CC   protein (BMP).
CC   Mature BMP can be produced by directly adding a BMP processing
CC   enzyme to a solution containing BMP precursor protein, or by
CC   transforming an animal cell with expression vectors containing DNA
CC   encoding the enzyme and precursor protein, culturing the
CC   transformant and isolating the mature BMP from the culture. The
CC   method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,
CC   which can be used to treat bone formation or regeneration
CC   abnormalities.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1e-58;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 11
AAW19210
ID   AAW19210 standard; Protein; 501 AA.
XX
AC   AAW19210;
XX
DT   04-MAR-1998  (first entry)
XX
DE   Human TGF-beta protein MP52.
XX
KW   Human transforming growth factor-beta; TGF-beta; MP52; superfamily;
KW   cartilage; bone inducing activity; inhibit; bone resorption.
XX
OS   Homo sapiens.
XX
PN   DE19548476-A1.
XX
PD   26-JUN-1997.
XX
PF   22-DEC-1995;   95DE-1048476.
XX
PR   22-DEC-1995;   95DE-1048476.
XX
PA   (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI   Bechtold R,  Hotten G,  Paulista M,  Pohl J,  Hoetten G;
XX
DR   WPI; 1997-333931/31.
DR   N-PSDB; AAT69695.
XX
PT   Compound containing protein from TGF-beta superfamily - has bone
PT   and/or cartilage inducing activity, useful in treatment of, e.g.
PT   osteoporosis, bone damage, Paget's disease and osteoarthritis
XX
PS   Claim 3; Page 9; 10pp; German.
XX
CC   This sequence is the human transforming growth factor (TGF)-beta protein
CC   designated MP52. MP52 can be used in a compound of formula (I):
CC   A-X(1-20)-B(1-20) (I); A = protein, or fragment, of the TGF-beta
CC   superfamily with cartilage and/or bone inducing activity (e.g. MP52);
CC   B = 1 or more substituent groups with an affinity to the extracellular
CC   matrix, cellular components of bone and/or cartilage and/or to a
CC   biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer
CC   groups. The compound may be used to inhibit bone resorption, prevent or
CC   treat bone or cartilage related disorders, including osteoporosis,
CC   Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and
CC   to treat bone or cartilage damage caused by wounding or overloading.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1e-58;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
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RESULT 12
AAW11900
ID   AAW11900 standard; Protein; 501 AA.
XX
AC   AAW11900;
XX
DT   28-OCT-1997  (first entry)
XX
DE   Human high mol. wt. protein MP52, a growth/differentiation factor.
XX
KW   Growth factor; diferentiation; bone induction; osteoporosis; teeth;
KW   tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW   wound healing; regeneration; skeletal disorder; fracture; dimer.
XX
OS   Homo sapiens.
XX
PN   WO9704095-A1.
XX
PD   06-FEB-1997.
XX
PF   24-JUL-1996;   96WO-JP02065.
XX
PR   24-JUL-1995;   95JP-0218022.
XX
PA   (FARH ) HOECHST JAPAN LTD.
PA   (FARH ) HOECHST PHARM & CHEM KK.
XX
PI   Fujino Y,  Kawai S,  Kimura M,  Matsumoto T,  Takahashi M;
XX
DR   WPI; 1997-132636/12.
DR   N-PSDB; AAT61412.
XX
PT   High molecular weight human MP52 growth or differentiation factor -
PT   promotes bone induction, is useful for treatment and prevention of
PT   bone disease
XX
PS   Claim 1; Page 12-16; 25pp; Japanese.
XX
CC   AAW11900 is a high mol. wt. form of a human growth/differentiation
CC   factor MP52. MP52 promotes bone induction and is useful for plastic
CC   reconstructive surgery, cosmetic facial treatment, bone transplantation
CC   and tooth implantation.  It is also useful  for the treatment and
CC   prevention of disorders of bone formation, bone, cartilage, joint
CC   tissue, skin, mucous membranes, nails or teeth; for wound treatment and
CC   tissue regeneration; and for the treatment of skeletal disorders and
CC   fractures.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1e-58;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 13
AAW01799
ID   AAW01799 standard; Protein; 501 AA.
XX
AC   AAW01799;
XX
DT   15-OCT-1997  (first entry)
XX
DE   Human MP52 protein.
XX
KW   Human; MP52; transforming growth factor; TGF; beta; medicament;
KW   treatment; prevention; nervous system; disease; neuropathology;
KW   ageing.
XX
OS   Homo sapiens.
XX
PN   DE19525416-A1.
XX
PD   16-JAN-1997.
XX
PF   12-JUL-1995;   95DE-1025416.
XX
PR   12-JUL-1995;   95DE-1025416.
XX
PA   (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI   Bechtold R,  Hoetten G,  Paulista M,  Pohl J,  Unsicker K;
XX
DR   WPI; 1997-078343/08.
DR   N-PSDB; AAT59405.
XX
PT   Medicaments contg. protein MP52 - useful for treating neurological
PT   disorders
XX
PS   Claim 2; Pages 12-14; 21pp; German.
XX
CC   The present sequence is the human MP52 protein, which is
CC   described in WO 9316099 and 9504819 as a member of the human
CC   transforming growth factor beta superfamily. Active MP52 can be
CC   used in a medicament to treat and prevent nervous system diseases,
CC   and/or to treat neuropathological conditions caused by nervous
CC   system ageing.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 501;
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Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
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Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 14
AAW12770
ID   AAW12770 standard; Protein; 501 AA.
XX
AC   AAW12770;
XX
DT   11-MAY-1997  (first entry)
XX
DE   Human bone morphogenic factor MP52 Arg.
XX
KW   Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
KW   connective tissue; mucous membrane; epithelium; teeth;
KW   wound healing; vulnerary; tissue regeneration; osteoporosis;
KW   bone fracture; dental implant; osteoblast.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Cleavage-site   380..381
FT                   /note= "sequencing suggests MP52 Arg is processed
FT                         proteolytically at Arg380-Arg381"
FT   Cleavage-site   381..382
FT                   /note= "alternative cleavage site at Arg381-Ala382"
FT   Mat_protein     381..501
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FT                   /label= Mat_protein
FT                   /note= "mature MP52 Arg preferred for use in
FT                         compsns. of the invention"
XX
PN   WO9706254-A1.
XX
PD   20-FEB-1997.
XX
PF   02-AUG-1996;   96WO-EP03427.
XX
PR   03-AUG-1995;   95EP-0112241.
XX
PA   (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
XX
PI   Fujino Y,  Kawai S,  Kimura M,  Matsumoto T,  Takahashi M;
XX
DR   WPI; 1997-154261/14.
DR   N-PSDB; AAT59729.
XX
PT   New human bone morphogenic factor, MP52 Arg - used in the treatment
PT   of osteoporosis and bone fracture, and for promoting bone regrowth
XX
PS   Claim 1; Page 12-15; 26pp; English.
XX
CC   Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
CC   factor that induces formation of cartilage from undifferentiated
CC   mesenchymal cells and which stimulates the differentiation and
CC   maturation of osteoblasts.  It is effective for treating/preventing
CC   bone diseases caused by abnormal bone metabolism such as
CC   osteoporosis.  It also accelerates the healing of bone fractures,
CC   and is useful for orthopaedic reconstruction, bone transplantation,
CC   and dental therapeutics because of its bone morphogenetic activity.
CC   It is also effective for preventing/treating cartilage, skin,
CC   connective tissue, mucous membrane, teeth and epithelial disorders.
CC   Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells
CC   utilising an isolated DNA sequence (AAT59729) in plasmid pMSS99.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 18;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 1e-58;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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RESULT 15
AAW44868
ID   AAW44868 standard; protein; 501 AA.
XX
AC   AAW44868;
XX
DT   24-SEP-1998  (first entry)
XX
DE   TGF-beta superfamily subunit.
XX
KW   TGF-beta; calcium phsophate matrix; bioactive implant; parodontosis;
KW   bone replacement; cartilage; bone; fracture.
XX
OS   Synthetic.
XX
PN   DE19647853-A1.
XX
PD   20-MAY-1998.
XX
PF   19-NOV-1996;   96DE-1047853.
XX
PR   19-NOV-1996;   96DE-1047853.
XX
PA   (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
PA   (GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.
XX
PI   Heide H,  Pabst J,  Paulista M,  Pohl J;
XX
DR   WPI; 1998-287890/26.
XX
PT   Bioactive implant material for bone replacement - comprising
PT   osteogenic calcium phosphate matrix coated with protein
XX
PS   Claim 3; Page 8-10; 12pp; German.
XX
CC   The TGF-beta superfamily subunit can be used together with a calcium
CC   phsophate matrix to produce a bioactive implant material for bone
CC   replacement.  The implant has cartilage and/or bone-forming activity and
CC   can be used for local treatment of cartilage and/or bone diseases or
CC   damage caused by trauma, surgery, degeneration or overloading.  The
CC   implant can also be used for the treatment of bone defects, e.g.
CC   parodontosis or fractures and in cosmetic and plastic surgery for fixing
CC   mobile bones.
XX
SQ   Sequence   501 AA;

  Query Match             99.4%;  Score 645;  DB 19;  Length 501;
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  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	645	99.4	119	8	US-08-945-459A-1	Sequence 1, Appli
2	645	99.4	119	10	US-09-068-253-2	Sequence 2, Appli
3	645	99.4	119	12	US-10-365-231-1	Sequence 1, Appli
4	645	99.4	119	12	US-10-414-954-1	Sequence 1, Appli
5	645	99.4	120	10	US-09-945-182-4	Sequence 4, Appli
6	645	99.4	501	8	US-08-981-490B-1	Sequence 1, Appli
7	645	99.4	501	12	US-10-164-279-53	Sequence 53, Appl
8	645	99.4	501	12	US-10-356-513-1	Sequence 1, Appli
9	645	99.4	501	12	US-10-356-513-5	Sequence 5, Appli
10	640	98.6	119	10	US-09-880-708-13	Sequence 13, Appl
11	640	98.6	495	10	US-09-880-708-10	Sequence 10, Appl
12	639	98.5	502	10	US-09-813-398-37	Sequence 37, Appl
13	629	96.9	501	9	US-09-730-772-13	Sequence 13, Appl
14	629	96.9	501	9	US-09-735-849-13	Sequence 13, Appl
15	629	96.9	501	12	US-10-379-830-13	Sequence 13, Appl
16	629	96.9	501	12	US-09-574-819-13	Sequence 13, Appl
17	548	84.4	354	12	US-09-930-512-74	Sequence 74, Appl
18	540	83.2	321	10	US-09-945-182-26	Sequence 26, Appl
19	540	83.2	455	12	US-09-930-512-20	Sequence 20, Appl
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21	538	82.9	263	10	US-09-945-182-32	Sequence 32, Appl
22	528	81.4	436	9	US-09-730-772-14	Sequence 14, Appl
23	528	81.4	436	9	US-09-735-849-14	Sequence 14, Appl
24	528	81.4	436	12	US-10-379-830-14	Sequence 14, Appl
25	528	81.4	436	12	US-09-574-819-14	Sequence 14, Appl
26	528	81.4	436	12	US-10-164-279-57	Sequence 57, Appl
27	528	81.4	436	12	US-09-930-512-72	Sequence 72, Appl
28	527	81.2	413	12	US-09-930-512-76	Sequence 76, Appl
29	524	80.7	399	12	US-09-930-512-73	Sequence 73, Appl
30	524	80.7	412	12	US-09-930-512-75	Sequence 75, Appl
31	494	76.1	294	10	US-09-945-182-2	Sequence 2, Appli
32	494	76.1	388	10	US-09-945-182-34	Sequence 34, Appl
33	494	76.1	411	10	US-09-945-182-28	Sequence 28, Appl
34	494	76.1	450	15	US-10-188-246-12	Sequence 12, Appl
35	493	76.0	151	12	US-10-164-279-61	Sequence 61, Appl
36	489	75.3	240	10	US-09-945-182-30	Sequence 30, Appl
37	385	59.3	72	10	US-09-945-182-15	Sequence 15, Appl
38	348	53.6	72	10	US-09-945-182-13	Sequence 13, Appl
39	347	53.5	117	14	US-10-115-406-13	Sequence 13, Appl
40	347	53.5	117	15	US-10-154-333-15	Sequence 15, Appl
41	347	53.5	118	10	US-09-813-459-10	Sequence 10, Appl
42	347	53.5	118	10	US-09-859-211-37	Sequence 37, Appl
43	347	53.5	118	10	US-09-880-708-15	Sequence 15, Appl
44	347	53.5	118	11	US-09-872-856-37	Sequence 37, Appl
45	347	53.5	118	15	US-10-335-483-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-08-945-459A-1
; Sequence 1, Application US/08945459A
; Publication No. US20020102633A1
;  GENERAL INFORMATION:
;    APPLICANT:  MAKISHIMA, FUSAO; TAKAMATSU,
;    APPLICANT:  HIROYUKI; MIKI, HIDEO; KAWAI,
;    APPLICANT:  SHINJI; KIMURA, MICHIO; MATSUMOTO,
;    APPLICANT:  TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
;    APPLICANT:  KOICHI; SATOH, YUSUKE
;    TITLE OF INVENTION:  A NOVEL PROTEIN AND
;    TITLE OF INVENTION:  PROCESS FOR PREPARING THE SAME
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN, MUSERLIAN AND LUCAS
;      ADDRESSEE:  LLP
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MICROSOFT WORD 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/945,459A
;      FILING DATE:  09-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/01062
;      FILING DATE:  19-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP7/322403
;      FILING DATE:  17-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP7/93664
;      FILING DATE:  19-APR-1995
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  146.1275
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 AMINO ACIDS
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;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PEPTIDE
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMOSAPIENS
;      TISSUE TYPE:  FETUS
;    FEATURE:
;      NAME/KEY:  MP52
;      LOCATION:  383 TO 501
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RESULT 2
US-09-068-253-2
; Sequence 2, Application US/09068253
; Patent No. US20020168381A1
; GENERAL INFORMATION:
;  APPLICANT: SHIMURA, Takesada
;  APPLICANT:  TORIYAMA, Satsuki
;  TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
;  FILE REFERENCE: 146.1286
;  CURRENT APPLICATION NUMBER: US/09/068,253
;  CURRENT FILING DATE:  1998-06-09
;  PRIOR APPLICATION NUMBER: PCT/JP96/03333
;  PRIOR FILING DATE: 1996-11-14
;  PRIOR APPLICATION NUMBER: JP 7/322402
;  PRIOR FILING DATE: 1995-11-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-068-253-2

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; Sequence 1, Application US/10365231
; Publication No. US20030181378A1
;  GENERAL INFORMATION:
;       APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
;                  HIROYUKI; MIKI, HIDEO; KAWAI,
;                  SHINJI; KIMURA, MICHIO; MATSUMOTO,
;                  TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
;                  KOICHI; SATOH, YUSUKE
;       TITLE OF INVENTION: A NOVEL PROTEIN AND
;                           PROCESS FOR PREPARING THE SAME
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
;                       LLP
;            STREET: 600 THIRD AVENUE
;            CITY: NEW YORK
;            STATE: NEW YORK
;            COUNTRY: USA
;            ZIP: 10016
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: FLOPPY DISK
;            COMPUTER: IBM PC COMPATIBLE
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MICROSOFT WORD 97
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/365,231
;            FILING DATE: 12-Feb-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/JP96/01062
;            FILING DATE: 19-APR-1996
;            APPLICATION NUMBER: JP7/322403
;            FILING DATE: 17-NOV-1995
;            APPLICATION NUMBER: JP7/93664
;            FILING DATE: 19-APR-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: CHARLES A. MUSERLIAN
;            REGISTRATION NUMBER: 19,683
;            REFERENCE/DOCKET NUMBER: 146.1275
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 661-8000
;            TELEFAX: (212) 661-8002
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 AMINO ACIDS
;            TYPE: AMINO ACID
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: LINEAR
;       MOLECULE TYPE: PEPTIDE
;       ORIGINAL SOURCE:
;            ORGANISM: HOMOSAPIENS
;            TISSUE TYPE: FETUS
;       FEATURE:
;            NAME/KEY:   MP52
;            LOCATION:   383 TO 501
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-365-231-1

  Query Match             99.4%;  Score 645;  DB 12;  Length 119;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-62;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 4
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US-10-414-954-1
; Sequence 1, Application US/10414954
; Publication No. US20040019185A1
; GENERAL INFORMATION:
;  APPLICANT: ANDOU, HIDETOSHI
;  APPLICANT:  HONDA, JUN
;  APPLICANT:  SUGIMOTO, SJUNJIRO
;  APPLICANT:  HOTTEN, GETRUD
;  APPLICANT:  BECHTOLD, ROLF
;  APPLICANT:  POHL, JENS
;  TITLE OF INVENTION: PROCESS FOR PREPARING PURIFIED ACTIVE MONOMER OF
;  TITLE OF INVENTION:  BONE-DERIVED FACTOR
;  FILE REFERENCE: 146.1320-1
;  CURRENT APPLICATION NUMBER: US/10/414,954
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 10/048,458
;  PRIOR FILING DATE: 2002-02-26
;  PRIOR APPLICATION NUMBER: 09/701,121
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: PCT/EP00/07600
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: 09/331,948
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: JP 10 141379
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: PCT/JP97/04784
;  PRIOR FILING DATE: 1997-12-24
;  PRIOR APPLICATION NUMBER: JP 8 355812
;  PRIOR FILING DATE: 1996-12-25
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human MP52
;   OTHER INFORMATION: variant
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (83)
;   OTHER INFORMATION: if dimeric human MP52 variant, Xaa is cysteine; if
;   OTHER INFORMATION: monomeric human MP52 variant, Xaa is any amino acid
;   OTHER INFORMATION: except cysteine and preferably alanine, serine,
;   OTHER INFORMATION: threonine, leucine, isoleucine, glycine or valine
US-10-414-954-1

  Query Match             99.4%;  Score 645;  DB 12;  Length 119;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-62;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTXCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 5
US-09-945-182-4
; Sequence 4, Application US/09945182
; Patent No. US20020160494A1
;   GENERAL INFORMATION:
;        APPLICANT: Celeste, Anthony J.
;                   Wozney, John
;                   Rosen, Vicki A.
;                   Wolfman, Neil
;                   Thomsen, Gerald H.
;                   Melton, Douglas A.
;        TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
;        NUMBER OF SEQUENCES: 35
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENETICS INSTITUTE, INC.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/945,182
;             FILING DATE: 31-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/808,324
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lazar, Steven R.
;             REGISTRATION NUMBER: 32,618
;             REFERENCE/DOCKET NUMBER: 5202-D
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617 498-8260
;             TELEFAX: 617 876-5851
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 120 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-945-182-4

  Query Match             99.4%;  Score 645;  DB 10;  Length 120;
  Best Local Similarity   99.2%;  Pred. No. 1.8e-62;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 6
US-08-981-490B-1
; Sequence 1, Application US/08981490B
; Publication No. US20020045568A1
; GENERAL INFORMATION:
;  APPLICANT: Hotten, Gertrud
;  APPLICANT:  Pohl, Jens
;  APPLICANT:  Bechtold, Rolf
;  APPLICANT:  Paulista, Michael
;  APPLICANT:  Unsicker, Klaus
;  TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
;  TITLE OF INVENTION:  NERVOUS SYSTEM
;  FILE REFERENCE: 100564-07032
;  CURRENT APPLICATION NUMBER: US/08/981,490B
;  CURRENT FILING DATE:  1998-05-18
;  PRIOR APPLICATION NUMBER: PCT/EP96/03065
;  PRIOR FILING DATE: 1996-07-12
;  PRIOR APPLICATION NUMBER: DE/195 25 416.3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-08-981-490B-1

Query Match 99.4%; Score 645; DB 8; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
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RESULT 7
US-10-164-279-53
; Sequence 53, Application US/10164279
; Publication No. US20030185792A1
; GENERAL INFORMATION:
; APPLICANT: Keck, P.
; TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
; FILE REFERENCE: CIBT-P04-566
; CURRENT APPLICATION NUMBER: US/10/164,279
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/791946
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-279-53

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
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RESULT 8
US-10-356-513-1
; Sequence 1, Application US/10356513
; Publication No. US20030220248A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
; TITLE OF INVENTION: The Nervous System
; FILE REFERENCE: 2923-0127
; CURRENT APPLICATION NUMBER: US/10/356,513
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 08/981490
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE 195 25 416 .3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Human
US-10-356-513-1

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
```

RESULT 9
US-10-356-513-5
; Sequence 5, Application US/10356513
; Publication No. US20030220248A1
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: The Use Of MP52 Or MP121 For Treating And Preventing Diseases Of
; TITLE OF INVENTION: The Nervous System
; FILE REFERENCE: 2923-0127
; CURRENT APPLICATION NUMBER: US/10/356,513
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 08/981490
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE 195 25 416 .3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Human
US-10-356-513-5

Query Match 99.4%; Score 645; DB 12; Length 501;
Best Local Similarity 99.2%; Pred. No. 9.2e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
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RESULT 10
US-09-880-708-13
; Sequence 13, Application US/09880708
; Patent No. US20020165361A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA

```
;             COUNTRY: USA
;             ZIP: 92121-2189
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/880,708
;             FILING DATE: 12-Jun-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/145,060
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/003,144
;             FILING DATE: 12-JAN-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lisa A. Haile, Ph.D.
;             REGISTRATION NUMBER: 38,347
;             REFERENCE/DOCKET NUMBER: 07265/057002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 858/677-1456
;             TELEFAX: 619/677-1465
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        IMMEDIATE SOURCE:
;             CLONE: GDF-5
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13

  Query Match             98.6%;  Score 640;  DB 10;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 6.3e-62;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 11
US-09-880-708-10
; Sequence 10, Application US/09880708
; Patent No. US20020165361A1
;   GENERAL INFORMATION:
;        APPLICANT: Lee, Se-Jin
;                   Huynh, Thanh
;        TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Gray Cary Ware & Freidenrich LLP
;             STREET: 4365 Executive Drive, Suite 1600
;             CITY: San Diego
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92121-2189
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/880,708
;             FILING DATE: 12-Jun-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/145,060
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/003,144
;             FILING DATE: 12-JAN-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lisa A. Haile, Ph.D.
;             REGISTRATION NUMBER: 38,347
;             REFERENCE/DOCKET NUMBER: 07265/057002
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 858/677-1456
;             TELEFAX: 619/677-1465
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 495 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-880-708-10

  Query Match             98.6%;  Score 640;  DB 10;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 3.2e-61;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 12
US-09-813-398-37
; Sequence 37, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
;  APPLICANT: Bruce D. Weintraub
;  APPLICANT:  Mariusz W. Szkudlinski
;  APPLICANT:  University of Maryland
;  TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
;  FILE REFERENCE: UOFMD.003C1
;  CURRENT APPLICATION NUMBER: US/09/813,398
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: PCT/US99/05908
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: PCT/US98/19772
;  PRIOR FILING DATE: 1998-09-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: HOMO SAPIEN
US-09-813-398-37

  Query Match             98.5%;  Score 639;  DB 10;  Length 502;
  Best Local Similarity   98.3%;  Pred. No. 4.1e-61;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 443

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        444 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 502


RESULT 13
US-09-730-772-13
; Sequence 13, Application US/09730772
; Patent No. US20010011131A1
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;  GENERAL INFORMATION:
;    APPLICANT:  Luyten, Frank P.
;    APPLICANT:  Moos, Jr., Malcolm
;    APPLICANT:  Chang, Steven Chao-Huan
;    TITLE OF INVENTION:  CARTILAGE-DERIVED MORPHOGENETIC
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive, 16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/730,772
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,081
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bartfeld, Neil S
;      REGISTRATION NUMBER:  39,901
;      REFERENCE/DOCKET NUMBER:  NIH099.001APC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  501 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-730-772-13

  Query Match             96.9%;  Score 629;  DB 9;  Length 501;
  Best Local Similarity   97.5%;  Pred. No. 5.1e-60;
  Matches  116;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              | |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        383 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFGCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 14
US-09-735-849-13
; Sequence 13, Application US/09735849
; Patent No. US20010037017A1
;  GENERAL INFORMATION:
;    APPLICANT:  Luyten, Frank P.
;    APPLICANT:  Moos, Jr., Malcolm
;    APPLICANT:  Chang, Steven Chao-Huan
;    TITLE OF INVENTION:  CARTILAGE-DERIVED MORPHOGENETIC
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive, 16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/735,849
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/836,081
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bartfeld, Neil S
;      REGISTRATION NUMBER:  39,901
;      REFERENCE/DOCKET NUMBER:  NIH099.001APC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  501 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-735-849-13

  Query Match             96.9%;  Score 629;  DB 9;  Length 501;
  Best Local Similarity   97.5%;  Pred. No. 5.1e-60;
  Matches  116;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
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Db        383 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFGCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 15
US-10-379-830-13
; Sequence 13, Application US/10379830
; Publication No. US20030176683A1
;  GENERAL INFORMATION:
;       APPLICANT: Luyten, Frank P.
;                  Moos, Jr., Malcolm
;                  Chang, Steven Chao-Huan
;       TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
;                           PROTEINS
;       NUMBER OF SEQUENCES: 24
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive, 16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/379,830
;            FILING DATE: 03-Mar-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/730,772
;            FILING DATE: 30-NOV-2000
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;             APPLICATION NUMBER: 08/836,081
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bartfeld, Neil S
;             REGISTRATION NUMBER: 39,901
;             REFERENCE/DOCKET NUMBER: NIH099.001APC
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-235-8550
;             TELEFAX: 619-235-0176
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 501 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-379-830-13

  Query Match             96.9%;  Score 629;  DB 12;  Length 501;
  Best Local Similarity   97.5%;  Pred. No. 5.1e-60;
  Matches  116;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              | ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        383 PSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFGCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


Search completed: February 18, 2004, 17:48:54
Job time : 34 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 17:41:20 ; Search time 21 Seconds
(without alignments)
239.762 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATRQGKRPSKNLKARCSR.....ANNVVYKQYEDMVVESCGCR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	645	99.4	120	1	US-08-362-670B-4	Sequence 4, Appli
2	645	99.4	120	3	US-08-333-576C-4	Sequence 4, Appli
3	645	99.4	120	3	US-08-808-324-4	Sequence 4, Appli
4	645	99.4	120	5	PCT-US94-14030A-4	Sequence 4, Appli
5	645	99.4	401	3	US-08-289-222E-3	Sequence 3, Appli
6	645	99.4	401	3	US-09-054-526B-3	Sequence 3, Appli
7	645	99.4	501	2	US-08-288-508C-2	Sequence 2, Appli
8	645	99.4	501	4	US-08-981-490B-1	Sequence 1, Appli
9	640	98.6	119	1	US-08-455-559-13	Sequence 13, Appl
10	640	98.6	119	3	US-09-145-060-13	Sequence 13, Appl
11	640	98.6	119	5	PCT-US94-00657-13	Sequence 13, Appl
12	640	98.6	495	1	US-08-455-559-10	Sequence 10, Appl
13	640	98.6	495	3	US-09-145-060-10	Sequence 10, Appl
14	640	98.6	495	5	PCT-US94-00657-10	Sequence 10, Appl
15	559	86.1	102	1	US-08-335-583C-51	Sequence 51, Appl
16	559	86.1	102	2	US-08-288-508C-13	Sequence 13, Appl
17	559	86.1	102	3	US-08-289-222E-22	Sequence 22, Appl
18	559	86.1	102	3	US-09-054-526B-22	Sequence 22, Appl
19	543	83.7	119	1	US-08-581-529B-7	Sequence 7, Appli
20	543	83.7	119	3	US-09-097-616-7	Sequence 7, Appli
21	543	83.7	119	5	PCT-US94-07762-7	Sequence 7, Appli
22	543	83.7	134	1	US-08-581-529B-6	Sequence 6, Appli
23	543	83.7	134	3	US-09-097-616-6	Sequence 6, Appli
24	543	83.7	134	5	PCT-US94-07762-6	Sequence 6, Appli
25	540	83.2	321	1	US-08-362-670B-26	Sequence 26, Appl
26	540	83.2	321	3	US-08-333-576C-26	Sequence 26, Appl
27	540	83.2	321	3	US-08-808-324-26	Sequence 26, Appl
28	540	83.2	321	5	PCT-US94-14030A-26	Sequence 26, Appl
29	538	82.9	263	1	US-08-362-670B-32	Sequence 32, Appl
30	538	82.9	263	3	US-08-333-576C-32	Sequence 32, Appl
31	538	82.9	263	3	US-08-808-324-32	Sequence 32, Appl
32	538	82.9	263	5	PCT-US94-14030A-32	Sequence 32, Appl
33	494	76.1	129	1	US-08-360-914B-15	Sequence 15, Appl
34	494	76.1	129	1	US-08-741-589A-13	Sequence 13, Appl
35	494	76.1	294	1	US-08-362-670B-2	Sequence 2, Appli
36	494	76.1	294	3	US-08-333-576C-2	Sequence 2, Appli
37	494	76.1	294	3	US-08-808-324-2	Sequence 2, Appli
38	494	76.1	294	5	PCT-US94-14030A-2	Sequence 2, Appli
39	494	76.1	388	1	US-08-362-670B-34	Sequence 34, Appl
40	494	76.1	388	3	US-08-333-576C-34	Sequence 34, Appl
41	494	76.1	388	3	US-08-808-324-34	Sequence 34, Appl
42	494	76.1	388	5	PCT-US94-14030A-34	Sequence 34, Appl
43	494	76.1	411	1	US-08-362-670B-28	Sequence 28, Appl
44	494	76.1	411	3	US-08-333-576C-28	Sequence 28, Appl
45	494	76.1	411	3	US-08-808-324-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-362-670B-4
; Sequence 4, Application US/08362670B
; Patent No. 5658882
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-670B-4

Query Match 99.4%; Score 645; DB 1; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

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Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
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Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 2
US-08-333-576C-4
; Sequence 4, Application US/08333576C
; Patent No. 6027919
;  GENERAL INFORMATION:
;    APPLICANT:  Celeste, Anthony J.
;    APPLICANT:  Wozney, John
;    APPLICANT:  Rosen, Vicki A.
;    APPLICANT:  Wolfman, Neil
;    APPLICANT:  Thomsen, Gerald H.
;    APPLICANT:  Melton, Douglas A.
;    TITLE OF INVENTION:  TENDON-INDUCING COMPOSITIONS
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENETICS INSTITUTE, INC.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/333,576C
;      FILING DATE:  No. 6027919ember 2, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lazar, Steven R.
;      REGISTRATION NUMBER:  32,618
;      REFERENCE/DOCKET NUMBER:  5202-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 498-8260
;      TELEFAX:  617 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-333-576C-4

  Query Match             99.4%;  Score 645;  DB 3;  Length 120;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
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Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 3
US-08-808-324-4
; Sequence 4, Application US/08808324
; Patent No. 6284872
;  GENERAL INFORMATION:
;    APPLICANT:  Celeste, Anthony J.
;    APPLICANT:  Wozney, John
;    APPLICANT:  Rosen, Vicki A.
;    APPLICANT:  Wolfman, Neil
;    APPLICANT:  Thomsen, Gerald H.
;    APPLICANT:  Melton, Douglas A.
;    TITLE OF INVENTION:  TENDON-INDUCING COMPOSITIONS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENETICS INSTITUTE, INC.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,324
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lazar, Steven R.
;      REGISTRATION NUMBER:  32,618
;      REFERENCE/DOCKET NUMBER:  5202-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 498-8260
;      TELEFAX:  617 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-808-324-4

  Query Match             99.4%;  Score 645;  DB 3;  Length 120;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 4
PCT-US94-14030A-4
; Sequence 4, Application PC/TUS9414030A
;  GENERAL INFORMATION:
;    APPLICANT:  GENETICS INSTITUTE, INC.
;    APPLICANT:  PRESIDENT AND FELLOWS OF HARVARD COLLEGE
;    TITLE OF INVENTION:  TENDON-INDUCING COMPOSITIONS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENETICS INSTITUTE, INC.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14030A
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  US 08/164,103
;       FILING DATE:  07-DEC-1993
;       APPLICATION NUMBER:  US 08/217,780
;       FILING DATE:  25-MAR-1994
;       APPLICATION NUMBER:  US 08/333,576
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lazar, Steven R.
;       REGISTRATION NUMBER:  32,618
;       REFERENCE/DOCKET NUMBER:  5202D-PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617 498-8260
;       TELEFAX:  617 876-5851
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  120 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US94-14030A-4

  Query Match             99.4%;  Score 645;  DB 5;  Length 120;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 61

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         62 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120


RESULT 5
US-08-289-222E-3
; Sequence 3, Application US/08289222E
; Patent No. 6120760
;  GENERAL INFORMATION:
;    APPLICANT:  HOTTEN, GERTRUD
;    APPLICANT:  NEIDHARDT, HELGE
;    APPLICANT:  BECHTOLD, ROLF
;    APPLICANT:  POHL, JENS
;    TITLE OF INVENTION:  GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
;    TITLE OF INVENTION:  FAMILY
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM
;      STREET:  655 FIFTEENTH STREET, N. W., G STREET LOBBY,
;      STREET:  SUITE 330
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/289,222E
;      FILING DATE:  25-AUG-1999
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/289,222
;      FILING DATE:  12-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 23 190.3
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EPO 92102324.8
;      FILING DATE:  12-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/00350
;      FILING DATE:  12-FEB-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, MONICA CHIN
;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P564-9021
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/638-5000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-289-222E-3

  Query Match             99.4%;  Score 645;  DB 3;  Length 401;
  Best Local Similarity   99.2%;  Pred. No. 6.2e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 342

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        343 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 401


RESULT 6
US-09-054-526B-3
; Sequence 3, Application US/09054526B
; Patent No. 6197550
;  GENERAL INFORMATION:
;    APPLICANT:  H TTEN, GERTRUD
;    APPLICANT:  NEIDHARDT, HELGE
;    APPLICANT:  BECHTOLD, ROLF
;    APPLICANT:  POHL, JENS
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING NOVEL
;    TITLE OF INVENTION:  GROWTH/DIFFERENTATION FACTORS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
;      STREET:  655 FIFTEENTH STREET, N. W., G STREET LOBBY,
;      STREET:  SUITE 330
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,526B
;      FILING DATE:  03-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/289,222
;      FILING DATE:  12-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 23 190.3
;      FILING DATE:  01-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EPO 92102324.8
;      FILING DATE:  12-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/00350
;      FILING DATE:  12-FEB-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITTS, MONICA CHIN
```

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;      REGISTRATION NUMBER:  36,105
;      REFERENCE/DOCKET NUMBER:  P564-8005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/638-5000
;      TELEFAX:  202/638-4810
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-054-526B-3

  Query Match             99.4%;  Score 645;  DB 3;  Length 401;
  Best Local Similarity   99.2%;  Pred. No. 6.2e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 342

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        343 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 401


RESULT 7
US-08-288-508C-2
; Sequence 2, Application US/08288508C
; Patent No. 5994094
;  GENERAL INFORMATION:
;    APPLICANT:  H tten, Gertrud
;    APPLICANT:  Neidhardt, Helge
;    APPLICANT:  Paulista, Michael
;    TITLE OF INVENTION:  NEW GROWTH/DIFFERENTIATING FACTOR OF
;    TITLE OF INVENTION:  THE TGF-  FAMILY
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/288,508C
;      FILING DATE:  10-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 26 829.3
;      FILING DATE:  10-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 18 222.8
;      FILING DATE:  25-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 20 157.5
;      FILING DATE:  09-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JAHNS, Kristina M.
;      REGISTRATION NUMBER:  P-41,092
;      REFERENCE/DOCKET NUMBER:  P564-4019
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-5000
;      TELEFAX:  (202)638-4810
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  501 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-288-508C-2

  Query Match             99.4%;  Score 645;  DB 2;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 8.3e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 8
US-08-981-490B-1
; Sequence 1, Application US/08981490B
; Patent No. 6531450
; GENERAL INFORMATION:
;  APPLICANT: Hotten, Gertrud
;  APPLICANT:  Pohl, Jens
;  APPLICANT:  Bechtold, Rolf
;  APPLICANT:  Paulista, Michael
;  APPLICANT:  Unsicker, Klaus
;  TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
;  TITLE OF INVENTION:  NERVOUS SYSTEM
;  FILE REFERENCE: 100564-07032
;  CURRENT APPLICATION NUMBER: US/08/981,490B
;  CURRENT FILING DATE:  1998-05-18
;  PRIOR APPLICATION NUMBER: PCT/EP96/03065
;  PRIOR FILING DATE: 1996-07-12
;  PRIOR APPLICATION NUMBER: DE/195 25 416.3
;  PRIOR FILING DATE: 1995-07-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-981-490B-1

  Query Match             99.4%;  Score 645;  DB 4;  Length 501;
  Best Local Similarity   99.2%;  Pred. No. 8.3e-64;
  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 442

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        443 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501


RESULT 9
US-08-455-559-13
; Sequence 13, Application US/08455559
; Patent No. 5801014
;  GENERAL INFORMATION:
;    APPLICANT:  LEE, SE-JIN
;    APPLICANT:  HUYNH, THANH
;    TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
;      STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
;      CITY:  LOS ANGELES
;      STATE:  CALIFORNIA
;      COUNTRY:  US
```

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;       ZIP:  90067
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/455,559
;       FILING DATE:  31-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/003,144
;       FILING DATE:  12-JAN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WETHERELL, JR. PH.D., JOHN R.
;       REGISTRATION NUMBER:  31,678
;       REFERENCE/DOCKET NUMBER:  PD2280
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/455-5100
;       TELEFAX:  619-455-5110
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     IMMEDIATE SOURCE:
;       CLONE:  GDF-5
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..119
US-08-455-559-13

  Query Match             98.6%;  Score 640;  DB 1;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 4.9e-64;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 10
US-09-145-060-13
; Sequence 13, Application US/09145060
; Patent No. 6245896
;  GENERAL INFORMATION:
;     APPLICANT:  Lee, Se-Jin
;     APPLICANT:  Huynh, Thanh
;     TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;     NUMBER OF SEQUENCES:  27
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  4225 Executive Square, Suite 1400
;       CITY:  La Jolla
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/145,060
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/455,559
;       FILING DATE:  31-MAY-1995
;       APPLICATION NUMBER:  08/003,144
;       FILING DATE:  12-JAN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lisa A. Haile, Ph.D.
;       REGISTRATION NUMBER:  38,347
;       REFERENCE/DOCKET NUMBER:  07265/057001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/678-5070
;       TELEFAX:  619/678-5099
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     IMMEDIATE SOURCE:
;       CLONE:  GDF-5
US-09-145-060-13

  Query Match             98.6%;  Score 640;  DB 3;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 4.9e-64;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 11
PCT-US94-00657-13
; Sequence 13, Application PC/TUS9400657
;  GENERAL INFORMATION:
;     APPLICANT:  SE-JIN LEE
;     APPLICANT:  HUYNH, THANH
;     TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;     NUMBER OF SEQUENCES:  27
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
;       STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
;       CITY:  LOS ANGELES
;       STATE:  CALIFORNIA
;       COUNTRY:  US
;       ZIP:  90067
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/00657
;       FILING DATE:  1/12/94
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WETHERELL, JR. PH.D., JOHN R.
;       REGISTRATION NUMBER:  31,678
;       REFERENCE/DOCKET NUMBER:  FD3256 CIP OF PD2280
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/455-5100
;       TELEFAX:  619-455-5110
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     IMMEDIATE SOURCE:
;       CLONE:  GDF-5
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;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
PCT-US94-00657-13

  Query Match             98.6%;  Score 640;  DB 5;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 4.9e-64;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119


RESULT 12
US-08-455-559-10
; Sequence 10, Application US/08455559
; Patent No. 5801014
;  GENERAL INFORMATION:
;    APPLICANT:  LEE, SE-JIN
;    APPLICANT:  HUYNH, THANH
;    TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
;      STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
;      CITY:  LOS ANGELES
;      STATE:  CALIFORNIA
;      COUNTRY:  US
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,559
;      FILING DATE:  31-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/003,144
;      FILING DATE:  12-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WETHERELL, JR. PH.D., JOHN R.
;      REGISTRATION NUMBER:  31,678
;      REFERENCE/DOCKET NUMBER:  PD2280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/455-5100
;      TELEFAX:  619-455-5110
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  495 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-455-559-10

  Query Match             98.6%;  Score 640;  DB 1;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 2.9e-63;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 13
US-09-145-060-10
; Sequence 10, Application US/09145060
; Patent No. 6245896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Se-Jin
;    APPLICANT:  Huynh, Thanh
;    TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/145,060
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/455,559
;      FILING DATE:  31-MAY-1995
;      APPLICATION NUMBER:  08/003,144
;      FILING DATE:  12-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lisa A. Haile, Ph.D.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/057001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  495 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-145-060-10

  Query Match             98.6%;  Score 640;  DB 3;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 2.9e-63;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 14
PCT-US94-00657-10
; Sequence 10, Application PC/TUS9400657
;  GENERAL INFORMATION:
;    APPLICANT:  SE-JIN LEE
;    APPLICANT:  HUYNH, THANH
;    TITLE OF INVENTION:  GROWTH DIFFERENTIATION FACTOR-5
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SPENSLEY HORN JUBAS & LUBITZ
;      STREET:  1880 CENTURY PARK EAST, FIFTH FLOOR
;      CITY:  LOS ANGELES
;      STATE:  CALIFORNIA
;      COUNTRY:  US
```

```
;       ZIP:  90067
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/00657
;       FILING DATE:  1/12/94
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WETHERELL, JR. PH.D., JOHN R.
;       REGISTRATION NUMBER:  31,678
;       REFERENCE/DOCKET NUMBER:  FD3256 CIP OF PD2280
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619/455-5100
;       TELEFAX:  619-455-5110
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  495 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US94-00657-10

  Query Match             98.6%;  Score 640;  DB 5;  Length 495;
  Best Local Similarity   98.3%;  Pred. No. 2.9e-63;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 PLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 436

Qy         61 PTNHAVIQTLMNSMDPESTPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        437 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 495


RESULT 15
US-08-335-583C-51
; Sequence 51, Application US/08335583C
; Patent No. 5693779
;  GENERAL INFORMATION:
;    APPLICANT:  Moos Jr., Malcolm
;    APPLICANT:  Wang, Shouwan
;    APPLICANT:  Krinks, Marie
;    TITLE OF INVENTION:  PRODUCTION AND USE OF
;    TITLE OF INVENTION:  ANTI-DORSALIZING MORPHOGENETIC PROTEIN
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson and Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,583C
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  NIH104.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  102 amino acids
;      TYPE:  amino acids
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  C-terminal
;    ORIGINAL SOURCE:
US-08-335-583C-51

  Query Match             86.1%;  Score 559;  DB 1;  Length 102;
  Best Local Similarity   99.0%;  Pred. No. 4.3e-55;
  Matches  101;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPE 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPE 60

Qy         78 STPPTACVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 119
              ||||| |||||||||||||||||||||||||||||||||||||
Db         61 STPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 102


Search completed: February 18, 2004, 17:44:26
Job time : 21 secs
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